

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 105953

TO: Karen A Lacourciere

Location: CM-1/11D09/11E12

Art Unit: 1635

Wednesday, October 15, 2003

Case Serial Number: 09/915543

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Lacourciere,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

From:

Sent:

Lacourciere, Karen Tuesday, October 14, 2003 3:13 PM STIC-Biotech/ChemLib Sequence search request 09/915,543

To:

Subject:

Please perform the following sequence searches for 09/915,543 in the commercial databases, pre-grant pubs and pending files (interference)

- 1) Residues 177-204 of SEQ ID NO:15
- 2) Residues 349-383 of SEQ ID NO:15
- 3) Residues 199-392 of SEQ ID NO:15

Thank-you!

Karen A. Lacourciere Ph.D.

CM1 11D09 GAU 1635

(703) 308-7523 mailbox 11E12

Steward Francis Technical Info. Specialica STIC/Riviagh ON 5800 TO 305-9200

Searcher:
Phone:
Location:
Date Picked Up: 10/15/10/
Date Completed: 5 / Fig. 2 Searcher Prep/Review:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 3
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	(1)
www/Internet:_	
Other (modifie)	



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Vol	luntary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
A	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	mments:

Dropoifor sand completed forms to STC/Blotterit Cham Library CMI — Circ. Desk.



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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5.1.6
Compugen Ltd
GenCore version
Copyright (c) 1993 - 2003
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; Search time 17.214 Seconds (without alignments) 258.182 Million cell updates/sec - protein search, using sw model OM protein

October 15, 2003, 10:27:32

Run on:

US-09-915-543-15_COPY_177_204 136 1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28

Title: Perfect score:

Scoring table: Sequence:

62 10.0 , Gapext 0.5 BLOSUM6 Gapop 1

1107863 seqs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

1: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
10: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* eseq_19Jun03:*

'SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMADTER

Result No.	Score 136	Query Match	% Query Ore Match Length DB 136 100.0 1426 23	DB 23	SUMMARLES ID AAB71229	Description Human legless homo
7	136	100.0		22	ABB11808	Human BCL9 homolog
m	129	94.5		22	AAO05855	Human polypeptide
4	86	72.1		22	ABB58779	Drosophila melanog
S	96	72.1		23	AAB71228	D. melanogaster 1g
9	94	69.1		23	AAU78460	Mouse beta-catenin
7	91	99		23	ABP06595	Human ORFX protein
80	29	49.3		23	AAU78461	Mouse beta-catenin
თ	65	47.8		22	AAO07544	Human polypeptide

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AAG3344 AAG3344 AAG3344 ABB6038 ABB8979 ABG1508	AAB43 ABB08 ABP66 ABJ25 ABJ25 ABJ26 AAG17 AAG17	AAG49 AAG17 AAG40 AAG40 AAG39 AAG40 AAG39 AAG39 AAG39	ABB70889 ABG04882 AAG08467 AAG1008 AAG1008 AAG08465 AAG08465 AAG81007 AAY77970 AAG81903 AAG83066
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0 0 0 0 10 10 10 10	01 01 01 02 02 10 10 10	OO 00 44 44 44 44 44 44 44 44 44 44 44 44	333 322.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.
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11 12 13 13 14 15 15	117 118 20 22 23 24	22 22 22 22 22 22 22 22 22 22 22 22 22	к к к к к к к к к к к к к к к к к к к

ALIGNMENTS

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Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                        Human legless homologue lgs/bc19 protein.
         AAB71229 standard; Protein; 1426 AA
                                                                                                                                                                                                                 27-JUL-2001; 2001US-0915543
                                                   18-NOV-2002 (first entry)
                                                                                                                                                                      US2002086986-A1.
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                            04-JUL-2002.
                              AAB71229;
AAB71229
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28-JUL-2000; 2000US-221502P (BASL/) BASLER K. (BRUN/) BRUNNER E. (FROE/) FROESCH B. (KRAM/) KRAMPS T. (PETE/) PETER O.

Peter 0; Kramps T, Froesch B, Brunner E, Basler K,

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                           This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue 1gs/bcl9 described in the
                                                                     useful in therapeutic method for treating disorders
                                                                                         as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 136; DB 23; Best Local Similarity 100.0%; Pred. No. 2.9e-12; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BCL9 homologue, SEQ ID NO:2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB11808 standard; peptide; 1435 AA.
                                                                                                                              B; 41pp; English.
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27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
              WPI; 2002-635689/68.
N-PSDB; AAF88467.
                                                                                                                                                                                                                                                                                                                                                                                                                            1426 AA;
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                                                                     Novel polypeptide
of cell fate such
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disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VYVESTEM
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                                                                                                                           Example II; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB11808,
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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ABB11808
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Gaps

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The convention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. Invention and the polypeptides, methods of detecting the nucleotides or the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence controlly an insight into their probable biological activities, and hence optential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell family and insight into their publications. The polypeptides of the invention may have various activities, stem cell growth factor activity; inmunomodulatory activity; activity; tissue growth activity; in may be concerned activities, and activities or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC differation or their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid and promail activities, properties, polypeptides and nucleotides and succerned in general ischaemia bone disorders (e.g., myeloid or lymphoid cell growth. Polypeptides involved with tissue regeneration and repair or proliferative retinopathy, atterosclerosis, corceary heart disease, arterial ischaemia bone disorders (e.g., myeloid or lymphoid cell growth. Polypeptides involved with tissue regeneration and repair or proliferative retinopathy, atterosclerosis, corceary heart disease.

CC disorders), chord in conceding them) may be used to promote wound fungal infections in addition to immune disease or accidental damage. The polypeptides and nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                            Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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thes 0;
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100.0%; Pred. No. 2.9
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                    Claim 20; Page 256-257; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO05855 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 19747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                        e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
ses 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1435 AA;
                   N-PSDB; ABA09052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA005855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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(PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                NO 19747; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 3129.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 129; DB 22;
Pred. No. 2.3e-12;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VYVFSTEMANKAAEAVLKGOVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 VYVFSTEMANKAAKAVLKGQVETMVSFH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB58779 standard; Protein; 1429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.9%;
Matches 26; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
                                                                                                                                     Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                             WO-US04927
                                                                                28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                           140 AA;
                                                             26-FEB-2001; 2001
                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                        WPI; 2001-514838,
N-PSDB; AAI85786
                                                                                                                                    Tang YT, Liu C,
                                                                                                                                                                                                                                Claim 20; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2.
                     W0200164835-A2
 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                          07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB58779;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legless; fruitfly; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3129; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 72.1%; Score 98; DB 22; Length 1429; Local Similarity 57.1%; Pred. No. 2.8e-06; Loservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peter 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kramps T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||||::||| ||::|| || ::||
323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VYVFSTEMANKAAEAVLKGOVETIVSFH 28
Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB71228 standard; Protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Froesch B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D. melanogaster lgs protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000US-221502P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-635689/68.
N-PSDB; AAF88466.
Venter JC, Adams M,
                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KRAM/) KRAMPS T. (PETE/) PETER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002086986-A1.
                                                                                           N-PSDB; ABL02882
                                                                                                                                                                                                                                 interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB71228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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1494 AA;

Sequence

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This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the prosophila melanogaster (fruitfly) legless (1gs) protein described in
useful in therapeutic method for treating disorders as cell differentiation or cell proliferation
                                                                                                                                                         41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                         Example II; Fig 2;
   Novel polypeptide of cell fate such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the disclosure of
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1464 Sequence

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Gaps
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 Length 1464;
                          3; Indels
72.1%; Score 98; DB 23; 57.1%; Pred. No. 2.9e-06;
                          Mismatches
                          .
0
                         Conservative
              Similarity
Query Match
Best Local Sim
Matches 16;
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::||||::||| ||:|| || :|| 345 318 IFVFSTQLANKGAESVLSGQFQTIIAYH 345 1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28 qq

AAU78460 standard; Protein; 1494 AA. AAU78460; RESULT 6 AAU78460

Mouse beta-catenin nuclear localised protein. (first entry) 02-JUL-2002

Mouse; beta-catenin nuclear localised protein; cancer;

; expressed sequence tag. gene therapy;

musculus Mus WO200224738-A1

28-MAR-2002.

WO-JP08140. 19-SEP-2001; 2001

22-SEP-2000; 2000JP-0287876

(KYOW) KYOWA HAKKO KOGYO KK

T, Adachi S; Akiyama

/36. WPI; 2002-330014/ N-PSDB; ABK47631. nuclear localised protein for diagnosis and treatment stated with nuclear localisation of beta-catenin e.g. New beta-catenin of diseases assoc beta-catenin cancer

-88; 113pp; Japanese. Page 81 lates to a beta-catenin nuclear localised protein the protein. The protein and encoding DNA are agnosis and treatment of diseases associated with tion of beta-catenin e.g. cancer, including gene sent sequence represents the amino acid sequence of in nuclear localised protein. applicable in diagnoclear localisati The invention reland DNA encoding mouse beta-caten

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                                    Gaps
                                    ő
            Length 1494;
                                   Indels
          69.1%; Score 94; DB 23; L, 60.7%; Pred. No. 1.3e-05; Live 8; Mismatches 3;
                                                                      1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                       ABP06595 standard; Protein; 114 AA
                                   Conservative
Query Match
Best Local Similarity
                                                                                                                    RESULT 7
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; Human ORFX protein sequence SEQ ID NO:13172. myasthenia gravis.

(first entry)

25-JUN-2002

Homo sapiens.

WO200192523-A2.

06-DEC-2001

29-MAY-2001; 2001WO-US10836.

30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach MD;

WPI; 2002-106308/14. N-PSDB; ABN22347 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders

Disclosure; SEQ ID 13172; 1037pp; English.

The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table I
in the specification). ABN15762 to ABN27252 encode the human ORFX

c proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
treating or preventing a pathology associated with an ORFX-associated
disorder in humans, and in the manufacture of a medicament for treating a
syndrome associated with ORFX-associated disorder. ORFX polynucleotide
sequences can be used in gene therapy. ORFX sequences can be used in generative disorders, haemorrhage,
c steoarthritis, neurodegenerative disorders, disorders mellitus, systemic
transplantation, cardiovascular diseases, diabetes mellitus, systemic
storage disease, various immune deficiencies and disorders, infectious
diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
disease and autoimmune inflammatory eye disease. ORFX proteins are also
useful for treating burns, incisions, ulcers, for treating osteoporosis,
bone degenerative disorders, or periodontal disease, and for gut

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ΩD QY

AAO07544 standard; Protein; 113 AA

AAO07544

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protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear localised protein for diagnosis and treatment ciated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 67; DB 23; Length 320; 57.1%; Pred. No. 0.035; tive 7; Mismatches 2; Indels
                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                             Score 91; DB 23; Length Pred. No. 1.7e-06; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse, beta-catenin nuclear localised protein; cancer; gene therapy, EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse beta-catenin nuclear localised protein #2.
                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                          1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -92; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78461 standard; Protein; 320 AA.
                                                                                                                                                                                      66.9%; Scu.
57.1%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO-JP08140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-2000; 2000JP-0287876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA;
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                              114 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABK47632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200224738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78461;
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The invention relates to human polynucleotides (AA.179941-AA.193841) and the encoded proteins (AA.000010-AA.013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 21436; 1399pp + Sequence Listing; English.
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Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays protein fragment SEQ ID NO: 40525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG33446 standard; Protein; 360 AA
                                                                    Human polypeptide SEQ ID NO 21436.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT;
                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
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Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA;
                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI87475
                                                                                                                                                                                                                               WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation,
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2000
                                  06-NOV-2001
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AAO07544;
                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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Gaps

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8 MANKAAEAVLKGQVETIVSFH 28

RESULT

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn. 990S-0135124.
990S-0135353.
990S-0135353.
990S-0135629.
990S-0137222.
990S-0137222.
990S-0137224.
990S-013724.
990S-013724.
990S-0139452.
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990S-0125288.
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990S-0128714.
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990S-0134218.
990S-0134256.
990S-0138455.
990S-0139455.
990S-0139455.
990S-0139455. 2000EP-0301439 dsqns 25-FEB-1999; 05-MAR-1999; 23-MAR-1999; 23-MAR-1999; 25-MAR-1999; 25-MAR-1999; 06-APR-1999; 06-APR-1999; 06-APR-1999; 06-APR-1999; 06-MAY-1999; 06-MA 25-FEB-2000; 06-SEP-2000 mays Zea

990S-0140353.
990US-0140354.
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990US-0140823.
990US-0141842.
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990US-0142052.
990US-0144333.
990US-0144933.
990US-014993.
990US-014993.
990US-014993.
990US-014993. 23-JUN-1999; 24-JUN-1999; 28-JUN-1999; 30-JUN-1999; 30-JUL-1999; 01-JUL-1999; 06-JUL-1999; 08-JUL-1999; 13-JUL-1999; 13-JUL-1999; 14-JUL-1999; 14-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 29-JUL-1999; 29-JUL-1999; 20-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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990S-0121825

990S-0123180.

990S-0125788.

990S-012624.

990S-0126234.

990S-0128234.

990S-0128234.

990S-0130891.

990S-0130891.

990S-0130489.

990S-0132486.

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990S - 0138094

990S - 0138119

990S - 0139452

990S - 0139452

990S - 0139453

990S - 0139456

990S - 0139456

990S - 0139456

990S - 0139460

990S - 0139460

990S - 0139460
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990S-0136782.
990S-0137222.
990S-0137528.
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99US-0139763.
99US-0139817.
99US-0140353.
99US-0140354.
                                       2000EP-0301439
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99US-0141842
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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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09-MAR-19999

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20-APR-19999

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                                       25-FEB-2000;
    EP1033405-A2
                    06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB Pred. No. 9.4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment SEQ ID NO: 40524.
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FSTRLANNLENLVLKEGPETIAAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSTEMANKAAEAVLKGQVETIVSF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 448 AA
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990S-0151438

990S-0152363.

990S-0152363.

990S-0152363.

990S-0154018.

990S-0154018.

990S-0155486.

990S-0155486.

990S-0155886.

990S-015596.

990S-015929.

990S-016088.

990S-016098.

990S-016098.

990S-016098.

990S-0161406.

990S-0161406.

990S-0161359.

990S-0161360.
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Best Local Similarity 50.0%;
Matches 12; Conservative
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31-Aug-1999)
01-SEP-1999;
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AAG33445
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KW hybri
KW hybri
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PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142920.

PR 10-JUL-1999; 99US-0142920.

PR 11-JUL-1999; 99US-0142920.

PR 11-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-01442920.

PR 15-JUL-1999; 99US-0144082.

PR 15-JUL-1999; 99US-0144082.

PR 19-JUL-1999; 99US-0144082.

PR 19-JUL-1999; 99US-0144333.

PR 20-JUL-1999; 99US-0144333.

PR 20-JUL-1999; 99US-0144333.

PR 20-JUL-1999; 99US-0144884.

PR 22-JUL-1999; 99US-0144884.

PR 23-JUL-1999; 99US-0144884.

PR 24-JUL-1999; 99US-014491.

PR 24-JUL-1999; 99US-01499.

PR 24-JUL-1999; 99US-01599.

PR 24-JUL-1999; 99US-01499.

PR 24-JUL-1999; 99US-01599.

PR 24-JUL-1999; 99US-01599.

PR 24-JUL-1999; 99US-01599.

PR 24-JUL-1999; 99US-01599.

PR 24
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                        4 FSTEMANKAAEAVLKGQVETIVSF 27
                                                                                                                                                                                                                                                                                                                                                                                                                    AAG33444 standard; Protein; 509 AA.
99US-0155139.
99US-0155139.
99US-0155486.
99US-0155659.
99US-0155458.
99US-0157117.
99US-0157117.
99US-015723.
99US-015923.
99US-015923.
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99US-015923.
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990S-0160989.
990S-0161406.
99US-0161406.
99US-0161359.
99US-0161359.
99US-0161351.
99US-0161920.
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Best Local Similarity 50.0%;
Matches 12; Conservative
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28-OCT-1999;
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        22-SEP-1999;
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24-SEP-1999;
29-SEP-1999;
04-OCT-1999;
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08-OCT-1999;
12-OCT-1999;
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2-0CT-1999;
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25-OCT-1999;
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AAG33444
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30S - 0123180 30S - 0123548 30S - 0125788 30S - 0126264 30S - 0126264 30S - 0126234 30S - 01287462 30S - 0129845 30S - 0130677 30S - 0130891 30S - 0130891 30S - 0130846 30S - 0130846 30S - 0130846 30S - 0130846 30S - 0130846	90.5. 90	990S-013884/. 990S-013984/. 990S-0139452. 990S-0139453. 990S-0139454. 990S-0139456. 990S-0139456. 990S-0139460. 990S-0139461. 990S-0139461. 990S-0139461. 990S-0139461. 990S-0139461. 990S-013999. 990S-0140891. 990S-0140891. 990S-0141287. 990S-014287.	9US-0142977 9US-0143542
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99US-0144605. 99US-0144085. 99US-0144086. 99US-0144331. 99US-0144331. 99US-0144331. 99US-0144334. 99US-0144334. 99US-0144632. 99US-0144632. 99US-0146612. 99US-0145086. 99US-0145089. 99US-014518. 99US-014518. 99US-014518. 99US-014518. 99US-014518. 99US-014518. 99US-014518. 99US-014518. 99US-0145919. 99US-0146388. 99US-0146388. 99US-0147204. 99US-0147302. 99US-0147302. 99US-0147303.	90.5 - 0.14 / 4 / 4 / 4 / 4 / 4 / 4 / 4 / 4 / 4 /
PR 14-JUL-1999; PR 15-JUL-1999; PR 16-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 20-JUL-1999; PR 20-JUL-1999; PR 20-JUL-1999; PR 21-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 23-JUL-1999; PR 27-JUL-1999; PR 27-JUL-1999; PR 27-JUL-1999; PR 27-JUL-1999; PR 02-AUG-1999; PR 02-AUG-1999; PR 03-AUG-1999; PR 05-AUG-1999; PR 06-AUG-1999; PR 06-AUG-1999;	RR RR 11-AUG-1999999999999999999999999999999999999

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24-MAY-2002 (first entry)
                                                                                                                                                                                                 Local Similarity 40.7 tes 11; Conservative
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                                                                                                                                                                        1049 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200190304-A2
                           interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders -
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                                                                                                                                                                          Sednence
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                                                                                                                                                                                                                                                                                                            Score 52; DB 21; Length 509;
Pred. No. 14;
2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 7953.
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FSTRLANNLENLVLKEGPETIAAF 269
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99US-0157753.

99US-0157865.

99US-0158029.

99US-0158232.

99US-0159294.

99US-0159294.

99US-0159329.

99US-0159330.

99US-0159331.

99US-0159331.

99US-0159638.

99US-0160741.

99US-0160741.

99US-0160760.

99US-0160980.

99US-0160980.

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99US-0160980.

99US-0161404.

99US-0161359.

99US-0161360.

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99US-0161360.
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Best Local Similarity 50.0%;
Matches 12; Conservative
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11-JUL-2000; 2000US-0614150
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N-PSDB; ABL04490.
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05-0CT-1999;

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28-0CT-1999;

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ABB60387
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL57737-ABL30511), and the encoded proteins
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                               Disclosure; SEQ ID NO 7953; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 51; DB 22; Length 1049; 40.7%; Pred. No. 49; Live 5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB89793 standard; Protein; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 2169.
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isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant)agonists are useful
in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone
marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
(b) immune disorders e.g. Addison's disease, allergies, autoimmune
haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
disease, multiple sclerosis, rhewmatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemias;
(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                           36.8%; Score 50; DB 23; Length 130; 44.4%; Pred. No. 5.7;
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SARAAKAVESGALELSPSFH 93
                                                                                                                                                                                                                                                                                                                                                                                                                      2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #15079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Protein; 365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                           Query Match 36.8
Best Local Similarity 44.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /73.
                                                                                                                                                                                                                                                                                                       130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG15088 standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362
N-PSDB; AAS79275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG15088;
                                                                                                                                                                                                                                                                                                          Sequence
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ABG15088
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                           36.8%; Score 50; DB ilarity 29.6%; Pred. No. 20; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YVFAXPVCNASAKTIISGLTECLIHCH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 15, 2003, 10:30:22
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                              365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Job time : 21.214 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein October 15, 2003, 10:27:32; Search time 5.66537 Seconds (without alignments) 209.113 Million cell updates/sec Run on:

US-09-915-543-15_COPY_177_204 136 1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28

Title: Perfect score: Sequence:

10.0 , Gapext 0.5 Gapop

BLOSUM62

Scoring table:

seqs, 42310858 residues 328717 Searched:

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3, Appli	ત્રે	ď	37,		103,	93, A		93,	93,	93,	93,	93,		93,	93,	88,	88,	103,	210,	29737	219	8, A _I	11,	8, 7	20,	Sequence 2, Appli
	QI	US-09-080-983-3	08-060-	US-09-447-453-2	US-09-091-725-37	-660-	-36	US-08-484-223B-93	US-08-919-597-93	US-08-475-668A-93	US-08-485-551A-93	US-08-471-913A-93	US-08-485-264A-93	US-08-474-349A-93	2	0	-485-	ï	-354	US-09-732-210-103	-732-210-	US-09-252-991A-29737	-634-238-	US-09-934-901-8	US-09-627-376-11	1-28	US-09-775-932-20	US-08-844-085-2
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1	Match	34.6	32.4	32.4	•	31.6	•	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.2	30.5
	Score	47	44	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42	42	42	42	42	42	42	41.5	41.5
11.40	NO.	1	7	m	4	ഹ	9	2	80	S	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 5, Appli Sequence 9, Appli Sequence 5, Appli Sequence 43, Appl Sequence 649, Appl Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	
US-08-453-472-5 US-08-038-948-9 US-08-484-993B-43 US-08-484-993B-43 US-08-484-158B-43 US-08-484-158B-43 US-08-484-158B-43 US-08-489-150A-43 US-08-149-223A-43 US-09-107-532A-5449 US-09-107-532A-5449 US-09-107-532A-6589 US-09-107-532A-6589	US-09-107-532A-5806 US-09-499-964-1
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226666888888884444 800012846078800128	44 45 5

ALIGNMENTS

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                                       Sequence 3, Application US/09080983
Patent No. 6197948
GENERAL INFORMATION:
APPLICANT: Zhu, Hai-Ying
APPLICANT: Ling, Kai-Shu
APPLICANT: Gonsalves, Dennis
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS TYPE 2 PROTEINS
TITLE OF INVENTION: AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 3; Length 2639;
Pred. No. 1.3e+02;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,983
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECORMONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2639 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.6%;
Best Local Similarity 33.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-080-83-3
RESULT 1
US-09-080-983-3
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Gaps

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RESULT 4
US-09-091-725-37
                                  COUNTRY:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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Uses
                                                                                                                                                                                                    Mitofusin Genes and their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                    APPLICANT: Fuller, Margaret
APPLICANT: Fuller, Margaret
APPLICANT: Hales, Karen
TITLE OF INVENTION: Mitofusin Genes and the
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: Bozicevic & Reed, LLP
285 Hamilton Avenue, Suite 200
                   403 YCFEELTEMTQRYGRCVLSDQIKTLI 428
2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                               ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,808
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YVFS - TEMANKAAEAVLKGQVETIV 25
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US-09-447-453-2
Sequence 2, Application US/09447453
Patent No. 6284507
GENERAL INFORMATION:
APPLICANT: Fuller, Margaret
APPLICANT: Hales, Karen
TITLE OF INVENTION: Mitofusin Gen
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:

''norreser: Bozicevic & Reed, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | DATA:
| GO/048,961
                                                                                                                     Sequence 2, Application US/09090808
Patent No. 6127159
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SUN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/04
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 718 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
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; TOPOLOGY: line
; MOLECULE TYPE: F
US-09-090-808-2
                                                                                     RESULT 2
US-09-090-808-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: United States of America
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.4%; Score 44; DB 3; Length 718; Best Local Similarity 34.6%; Pred. No. 79; Matches 9; Conservative 5; Mismatches 10; Indels
                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Improved methods for TITLE OF INVENTION: and recombinant DNA NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEB: Morrison & Foerster 11p
STREET: 2000 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YVFS--TEMANKAAEAVLKGQVETIV 25
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APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  US/09/447,453
                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/048,961
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SUN-63P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUN-63P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 37, Application US/09091725
; Patent No. 6329141
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-447-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                     COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2000 rem
Palo Alto
                                              USA
                                                                    94301
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APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, ComPositions M.
APPLICANT: Lambert, ComPositions M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Danis M.
APPLICANT: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                              Score 43; DB 4; Length 145;
Pred. No. 16;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                         STEMANKAA-EAVLKG-----QVETIVSFH 28
                                                                                                                                                                                                                                                                                 31.6%; Score 43; DB 36.4%; Pred. No. 63; tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:

(212) 790-9090

LINFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERIT

LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                      93, Application US/08486099, 6013263
                 35,492
              REGISTRATION NUMBER: 35,495
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                Query Match 31.6%;
Best Local Similarity 43.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                       LENGTH: 145 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-091-725-37
NAME: E. Victor Donahue
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Best Local Similarity 36.4
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93, Applicated Patent No. 6013263 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
; TOPOLOGY: unkr;
; MOLECULE TYPE: E
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US-08-486-099-93
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 63;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/360,107A FILING DATE: 20-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7872-013
                                Sequence 103, Application US/08360107A Patent No. 6017536 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :||| | : ||:::
41 SLEQSNKAIEEIREATQETVIA 62
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Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 STEMANKAAEAVLKGQVETIVS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolognesi, Dani P.
Matthews, Thomas J
                                                                                          Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                   Barney, Shawn O.
Lambert, Dennis M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 438 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36.*
** 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MOLECULE TYPE: protein US-08-360-107A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                          New York
RESULT 6
US-08-360-107A-103
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US-08-484-223B-93
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APPLICANT:
APPLICANT:
                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT:
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: TRANSMISSION
    Langlois, Alphonse J. Fertion: COMPOSITIONS FOR INHIBITION OF FUNCTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.6%; Score 43; DB 3; Length 438; 36.4%; Pred. No. 63; tive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,223B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                               STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pennie & Edmonds
5 Avenue of the Americas
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1, Laura A.
10,742
10,742
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: MEMBRANE FUSI
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 93, Application US/08919597 Patent No. 6054265 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2] 790-9090
869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: COLUZZÍ, LAUKA A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 787 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bolognesi, Da APPLICANT: Bolognesi, Da APPLICANT: Matthews, Tho APPLICANT: Matthews, Tho APPLICANT: Barney, Shawn APPLICANT: Barney, Stamma APPLICANT: Lambert, Denn APPLICANT: Lambert, Denn APPLICANT: Langlois, Alp TITLE OF INVENTION: METH TITLE OF INVENTION: OF M TITLE OF INVENTION: TRAN NUMBER OF SEQUENCES: 273 CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Ed STREET: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: anim.
STRANDEDNESS:
TOPOLOGY: unkr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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US-08-919-597-93
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Sequence 93, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 43; DB 3; Length 438; 36.4%; Pred. No. 63; tive 6; Mismatches 8; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/919,597
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....EK: US/08/475,668A
07-JUN-1995
JN: 424
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                              ATTORNEL/COLUZZI, LAURA A.
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7872-026
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :||| | : ||:::
41 SLEQSNKAIEEIREATQETVIA 62
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 STEMANKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                              : LELEFAX: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.*
Lace 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-919-597-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YOL.
STATE: NEW YOL.
COUNTRY: USA
TP: 10036-2711
TP: TPOABLE FY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
OPERATING SYSTEM:
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                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                    FILING DATE;
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Sequence 93, Application US/0848551A

Patent No. 6068973

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: RETGION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

ADDRESSE: Pennie & Edmonds LLP
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                                                                                                                          DB 3; Length 438;
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: USA-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                          Score 43; DB :
Pred. No. 63;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Pennie & Edmonds LLP
?: 1155 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/485,551A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7872-023
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SLEQSNKAIEEIREATQETVIA 62
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) 869-9741/8864
                                                                                                                          Query Match 31.6%; Sc
Best Local Similarity 36.4%; Pr
Matches 8; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE.
TELETAX: (212) 869-9/41/C-1ELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 36.4
B; Conservative
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MOLECULE TYPE:
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                                                                         ; MULECULE
US-08-475-668A-93
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-08-485-551A-93
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CITY: Ne
STATE: N
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Best Local S
Matches 8
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US-08-4
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING BPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 63;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 43; DE 36.4%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7872-030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 SLEQSNKAIEEIREATQETVIA 62
US-08-471-913A-93; Sequence 93, Application US/08471913A; Patent No. 6093794; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
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                                                                                       Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
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LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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TOPOLOGY: unknown
MOLECULE TYPE: proté
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                     APPLICANT:
                                                                                                               APPLICANT:
                                                                                           APPLICANT:
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MOLECULE TYPE: protein
    APPLICATION NUMBER:
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
    RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 43; DB 3; Length 438; 36.4%; Pred. No. 63; tive 6; Mismatches 8; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avenue of the Americas
                                                        SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 STEMANKAAEAVLKGQVETIVS 26
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SLEQSNKAIEEIREATQETVIA 62
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5. 6333395
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12) 869-9741/8864
1 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO: 93:
TITLE OF INVENTION: RESPIRATION NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the CITY: New York STATE: New York COUNTRY: USA ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.49
Matches 8; Conservative
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TOPOLOGY: unknown
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GENERAL INFORMATION
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TELEX: 66141 PINFORMATION FOR SEQ
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CORRESPONDENCE AL
ADDRESSEE: Per
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ZIP: 10036-27
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US-08-485-264A-93
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-474-349A-93
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Sequence 29, Application US/08255208A

Patent No. 6440656

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.6%; Score 43; DB 4; Length 438; Best Local Similarity 36.4%; Pred. No. 63; Matches 8; Conservative 6; Mismatches 8; Indels
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APPLICATION NUMBER: US/08/255,208A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
US/08/474,349A
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7872-010
                            FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 STEMANKAAEAVLKGQVETIVS 26
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 790-9090
(212) 869-9741/8864
5141 PENNIE
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NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 438 amino acids
amino acid
                                                                                                                                                                                                                                                                               LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-474-349A-93
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Patent No. 6479055

Patent No. 6479056

Patent No. 6479056

Patent No. 6479056

Patent No. 6479066

Patent No. 647066

Patent No. 6479066

Patent 
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                                                                       Query Match 31.6%; Score 43; DB 4; Length 438; Best Local Similarity 36.4%; Pred. No. 63; Matches 8; Conservative 6; Mismatches 8; Indels
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NAME: COCUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                            5 STEMANKAAEAVLKGQVETIVS 26
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SLEQSNKAIEEIREATQETVIA 62
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| SLEQSNKAIEEIREATQETVIA 62
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TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-93
                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-470-896-93
; Sequence 93, Applicati
...* No. 6479055
US-08-255-208A-29
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Search completed: October 15, 2003, 10:31:58 Job time : 6.66537 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Copyright (c) 1993 - 2003 Compugen from.

OM protein - protein search, using sw model

Run on: October 15, 2003, 10:32:06; Search time 11.8755 Seconds

(without alignments)

379.908 Million cell updates/sec

Title: US-09-915-543-15_COPY_177_204

Perfect score: 136

Sequence: 1 VYVESTEMANKAABAVLKGQVETIVSFH 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 600653 seqs, 161128416 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 3547, Ap	Sequence 8547, Ap	Sequence 6, Appli	Sequence 8, Appli	Sequence 10, Appl	Sequence 10721, A	Sequence 92, Appl	Sequence 9002, Ap	Sequence 10457, A	Sequence 2, Appli	Sequence 5144, Ap	Sequence 212, App
	GI.	US-10-322-579-3	US-10-322-579-15	US-10-322-579-2	US-10-128-714-3547	US-10-128-714-8547	US-10-008-355-6	US-10-167-547C-8	US-10-167-547C-10	US-10-156-761-10721	US-10-342-224-92	US-10-156-761-9002	US-09-815-242-10457	US-10-117-846-2	US-09-764-891-5144	US-10-306-762-212
	DB	15	15	15	15	15	14	12	12	15	12	15	σ	14	11	12
	Query Match Length DB ID	28	1426	28	984	1058	732	471	503	747	170	171	484	718	80	315
d	Query Match	100.0	100.0	72.1	36.0	36.0	34.6	33.8	33.1	33.1	32.7	32.4	32.4	32.4	31.6	31.6
	Score	136	136	86	49	49	47	46	45	45	44.5	44	44	44	43	43
	Result No.		7	m	4	īΟ	9	7	8	o,	10	11	12	13	14	15

RESULT 2 US-10-322-579-15

14 30 93 93 93	Sequence 8, Appli Sequence 18, Appl Sequence 8, Appli Sequence 42, Appl Sequence 42, Appl Sequence 9, Appli Sequence 11, Appli	224189114	Sequence 10636, A Sequence 10636, Ap Sequence 11478, A Sequence 59, Appl Sequence 1, Appli Sequence 393, App Sequence 393, App Sequence 37, Appl
12 US-10-032-585 11 US-09-951-061 12 US-10-097-111 15 US-10-156-761 15 US-10-156-761	358 10 US-09-934-901-8 358 10 US-09-934-868-18 358 12 US-10-320-874-8 350 12 US-10-320-924-8 380 12 US-10-183-708-42 380 12 US-09-932-227-42 399 12 US-10-293-971-9 541 14 US-10-047-676A-11	0 8 6 6 7 7 6 6 7 7 6 6 6 6 6 6 6 6 6 6 6	456 9 US-09-815-242-10636 516 10 US-09-738-626-5086 568 15 US-10-156-761-11478 638 15 US-10-234-432-59 689 14 US-10-052-664-1 689 15 US-10-097-340-221 693 9 US-09-741-669-393 727 15 US-10-234-432-30
43 31.6 42 30.9 42 30.9 42 30.9		41.55 4.44 4.15 4.15 4.15 4.15 4.15 4.15	441 441 441 441 441 441 441 441 441 441
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ALIGNMENTS

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RESULT 1

US-10-32-579-3

US-10-32-579-3

US-10-32-579-3

Sequence 3, Application US/1032579

Publication No. US20030114413a1

SEGURERAL INFORMATION:

APPLICANT: BASIER, Ronrad

APPLICANT: RENUNER: Enich

APPLICANT: FROMESCH, Barbara

APPLICANT: FROMESCH, Barbara

APPLICANT: FROMESCH, Barbara

APPLICANT: PROMESCH, DIN'S Enich

TITLE OF INVENTION: THERABUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

TITLE OF INVENTION: THERABUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

FILE REPERENCE: 060341

CURRENT FILING DATE: 2002-12-19

CURRENT FILING DATE: 2001-07-219

PRIOR APPLICATION NUMBER: US/09/915,543

PRIOR APPLICATION NUMBER: US/09/915,543

PRIOR PALICATION NUMBER: 060221,502

PRIOR PLICATION NUMBER: 060221,502

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 28

TENGTH: 2
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Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Mo
APPLICANT: Jiang, Mo
APPLICANT: Landy, Carlos
APPLICANT: Landy, Carlos
APPLICANT: Examulo, Carlos
APPLICANT: Examulo, Carlos
APPLICANT: Examulo, Carlos
APPLICANT: Examulo, Carlos
APPLICANT: Garlos
APPLICANT: Garlos
APPLICANT: Mothods of use
TITLE OF INVENTION: Mothods of use
FILE REFERENCE: 10182-018-99
CURRENT APPLICATION NUMBER: US /0/285,697
FRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
SEQ ID NO 3547
ERRORHE: Patentin version 3.1
SEQ ID NO 3547
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Sequence 847, Application US/2003011901341

GENERAL INFORMATION:

APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Lashkoff, Daniel
APPLICANT: Used Color-04-23
CURRENT FILING DATE: 2001-04-37

PRIOR FILING DATE: 2001-04-37

PRIOR FILING DATE: 2001-06-55

PRIOR FILING DATE: 2001-06-55

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SEQ ID NOS: 8603

SEQ ID NO 8547

TANGTH. 10 NO 8547
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: ||||: ||||| :: 500 VYRANMANKSAAAVLKSKL 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VFSTEMANKAAEAVLKGQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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                                                                                                                                                                           ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oliver: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
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Pred. No. 9.6e-09;
9; Mismatches 3; Indels
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9.4e-13;
hes 0;
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Pred. No. 9.4;
Mismatches
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APPLICANT: FROESCH, Barbara
APPLICANT: RRAMPS, Thomas
APPLICANT: PETER, Oliver
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COM
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOS
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/915,543
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
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NKGAESVLSGQFQTIIAYH 28
                                                                                                                                                                                                                                         NUMBER: US/10/322,579
: 2002-12-19
JMBER: US/09/915,543
2001-07-27
                                                                             APPLICANT: BASILER, NOILEAU
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: KRAMPS, Thomas
APPLICANT: KRAMPS, Thomas
APPLICANT: PETER, Oliver
TITLE OF INVENTION: ESSENTIAL DOWNSTREP
TITLE OF INVENTION: THERAPEUTIC AND DI
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,5
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
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   tion US/10322579
030114413A1
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Publication No. US20030114413A1
GENERAL INFORMATION:
APPLICANT: BASLER, Konrad
APPLICANT: BRUNNER, Erich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 28; Conservative 0;
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Barbara
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SEQ ID NO 2

LENGTH: 28

TYPE: PRT

ORGANISM: Drosophila lgs

US-10-322-579-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /bc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human lgs:
US-10-322-579-15
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Sequence 15, Applicat Publication No. US200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS SOFTWARE: Patentin v SEQ ID NO 15 LENGTH: 1426
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1 IFVFSTQLA
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                                                               APPLICANT: BASLER
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Best Local Simil
Matches 16; (
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US-10-322-579-2
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Sequence 10, Application US/10167547C
Publication No. US20030170653Al
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT APPLICATION NUMBER: 60/297198
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 10
LENGTH: 507
LENGTH: 507
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US-10-342-224-92
; Sequence 92, Application US/10342224
; Publication No. US20030162294A1
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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; Sequence 10721, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
; APPLICANT: SARAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-05-97
; PRIOR FILING DATE: 2001-05-97
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                                                                                                                                                                                                                                                                                                                                                                                                Score 45;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptomyces avermitilis
US-10-156-761-10721
                                                                                                                                                                                                                                                                                                                                                                                             33.1%;
ilarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.1%;
39.1%;
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Best Local Similarity
Matches 9, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
US-10-167-547C-10
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Publication No. US20030170653A1

GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C

CURRENT FILING DATE: 2003-03-17

PRIOR FILING DATE: 2001-06-08
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                                                                                                                                                                       RESULT 6
US-10-008-355-6
Sequence 6, Application US/10008355
Publication No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
              Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 732;
                                                    Indels
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           DB 15;
50;
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67:
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                             Pred. No. 50;
4; Mismatches
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Pred. No.
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Pred. No.
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AQEKAEKILAGKLST 539
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                                                                                                                 500 VYRANMANKSAAAVLKSKL 518
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          Query Match
Best Local Similarity 52.6%; Pr
Matches 10; Conservative 4;
                                                                                    3 VFSTEMANKAAEAVLKGQV 21
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41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.6%;
ilarity 39.1%;
Conservative
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; ORGANISM: tulip pistil
US-10-167-547C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft O
SEQ ID NO 8
LENGTH: 471
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

CORGANISM: Shewanel

US-10-008-355-6
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LENGTH: 732
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Best Local S
Matches 9
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INVENTION: Identification of Essential Genes in INVENTION: Prokarvotes
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US-10-117-846-2
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                                                                                                                                                                                                                                                                                   Length 170;
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                                                                                                                                                                                                                                                                                   DB 12;
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Pred. No. 35;
5; Mismatches 13;
FILE REFERENCE: CNN-012US

CURRENT APPLICATION NUMBER: US/10/342,224

CURRENT FILING DATE: 2003-01-13

PRIOR APPLICATION NUMBER: US/09/762,154

PRIOR FILING DATE: 2002-02-02

PRIOR FILING DATE: 1998-08-04

PRIOR FILING DATE: 1998-08-04

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 92

LENGTH: 170

TYPE: PRT
                                                                                                                                                                                                                                                                              32.7%; Score 44.5; I
y 52.0%; Pred. No. 29;
rvative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OWURA, SATOSHI

APPLICANT: OWURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: BHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: BATTORI, WASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

LENGHH: 171

"WATHER FILING DATE: 1001-08-02

LENGHH: 171
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-156-761-9002
Sequence 9002, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRGANISM: Streptomyces avermitilis
US-10-156-761-9002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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US-10-342-224-92
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
Yamamoto, Robert T
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ilarity 35.7%;
Conservative
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Best Local Similarity
Matches 13; Conser
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Best Local Similarity
Matches 10; Conser
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US-09-815-242-10457
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Publication No. US20020168673A1

GENERAL INFORMATION:

APPLICANT: Fuller, Margaret T

APPLICANT: Hales, Karen G.

TITLE OF INVENTION: Mitofusins, Fzo Homologs and Functional

TITLE OF INVENTION: Derivatives Thereof

FILE REFERENCE: STAN-063CIP3

CURRENT APPLICATION NUMBER: US/10/117,846

CURRENT FILING DATE: 2002-04-05

PRIOR PPLICATION NUMBER: 09/413,285

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 718

"LENGTH: 718

"WUPE: Day
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 9; Dems-Pred. No. 1.2e+02;
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-10-16

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10457

LENGTH: 484
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US-09-764-891-5144
; Sequence 5144, Application US/09764891
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-117-846-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Escherichia coli
US-09-815-242-10457
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Best Local Similarity 30.0
Matches 6; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5144
LENGTH: 80
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Sequence 212. Application US/10306762

Publication No. US20030187220A1

GENERAL INFORMATION:

APPLICANT: Park, Frances

APPLICANT: Gajiwala, Ketan S.

APPLICANT: Buchanan, Sean Grant

APPLICANT

APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.6%; Score 43; DB 11; Length 80; ilarity 34.8%; Pred. No. 20; Conservative 7; Mismatches 8; Indels
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46 MHIFSSEYANKPVTAISAMHMQT 68
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; ORGANISM: Homo sapi
US-09-764-891-5144
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Best Local Similarity
Matches 8; Conser
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US-10-306-762-212
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Search completed: October 15, 2003, 10:50:57 Job time: 13.8755 secs

||| ||| ||::|| |::|| 29 TEMI--VADAIIHGQREKLLGYH 49

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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- protein search, using sw model OM protein ; Search time 6.64591 Seconds (without alignments) 405.170 Million cell updates/sec October 15, 2003, 10:27:32 Run on:

US-09-915-543-15_COPY_177_204 136 1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28 BLOSUM62 Title: Perfect score: Sequence: Scoring table:

283308 seqs, 96168682 residues Searched:

0.5

Gapop 10.0 , Gapext

Total number of hits satisfying chosen parameters:

2000000000 0 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	s de la completa del completa de la completa del completa de la completa del completa de la completa del completa de la completa del completa de la completa del completa de la completa del complet	Ų		protein F17L21.2 [probable response	SqaT protein VCA02	probable D-2-hydro	dihydroxyacetone k	hypothetical prote	prolidase (Xaa-Pro	probable bacterion	hypothetical prote		in	probable aminotran	hypothetical prote	probable acetyl-Co	class II histocomp	qlutaconate CoA-tr	cellulase (EC 3.2.	ase -	hypothetical prote				n e	hypothetical prote		ρц
SUMMARIES	ΩI	I40812	T27465	G97070	D86398	F71315	D82484	C81380	E84074	T01822	F90179	AD0623	T29695	808500	C69962	E95887	F72308	855089	S04363	A99261	S54744	S39962	H72478	B96495	н96762	D90907	F85710	T43131	T14645	444
	DB	71	7	~	7	~	N	7	7	7	7	7	7	N	N	ď	N	N	(7	~	N	7	~	~	N	7	~	~	7	N
	Length	205	634	243	210	458	586	311	330	319	352	662	586	330	363	461	1289	2123	256	268	504	505	131	451	555	48	50	126	265	318
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	Score	09	55	51	49	49	49	48.5	48	47	47	Ť	46.5	46	46	46	46	4	ς.	S.		δ.	45	45	45	4	44.5	44	44	44
	Result No.	Н	7	m	4	5	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	29

hypothetical protein Y87G2A.m - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T27465
R; White, S.
Submitted to the EMBL Data Library, September 1999
A; Reference number: 220371
A; Reference number: 220371
A; Reference number: 220371
A; Reference number: 220371
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-634 <WIL>
A; Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54487.1; CESP:Y87G2A.m
A; Experimental source: clone Y87G2A
C; Genetics:
A; Genetics:
A; Gene: CESP:Y87G2A.m
A; Introns: 74/1; 270/1

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Gaps

; 0

Score 55; DB 2; Length 634; Pred. No. 4.2; 2; Mismatches 13; Indels

40.4%; ilarity 44.4%; Conservative

Query Match Best Local Similarity Matches 12; Conserva

phosphate carrier probable transposo	acriflavin resista	probable transport	hypothetical prote hypothetical 50 9	hypothetical prote	probable 1, 2-diacy	Vibriolysin (EC 3. probable DNA ligas	valine-tRNA liqase	polyketide synthas	hypothetical_prote	6.7-dimethol-A-rih	hypothetical prote
T19105 A85056	AH3455 A72498	AG1051	A86116 D65230	A98275	T05092	G72709	T39630	PN0637	T18644	T40440	AD3133
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32.4	32.4	32.4	32.4	32.4	3.2.8 4.4	32.4	32.4	32.4	31.5	31.6	31.6
4 4	† † † †	7 4	† 4	44	5	44	7 7	4, 4	4	43	43
30 31	3.8	34 35	36	37	20 On	40	41	4.	4.5	44	45

ALIGNMENTS

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porphobilinogen synthase (EC 4.2.1.24) - Clostridium josui (fragment)
N;Alternate names: delta-aminolevulinic acid dehydratase
C;Species: Clostridium josui
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: 140812
R;Fujino, E.; Fujino, T.; Karita, S.; Sakka, K.; Ohmiya, K.
J. Bacteriol. 177, 5169-5175, 1995
A;Title: Cloning and sequencing of some genes responsible for porphyrin biosynthesis
A;Reference number: A57344; MUID:95394829; PMID:7665501
A;Reference number: A57344; MUID:95394829; PMID:7665501
A;Reference number: A57344; MUID:95394829; PMID:7665501
A;Reference number: GB:D28503; NID:q536874; PIDN:BAA05863.1; PID:q556484
C;Genetics:
A;Cross-references: GB:D28503; NID:q536874; PIDN:BAA05863.1; PID:g556484
C;Genetics:
A;Gene: hemB
C;Superfamily: porphobilinogen synthase
C;Keywords: carbon-oxygen lyase; hydro-lyase
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Best Local Similarity 46.2%; Pred. No. 0.23;
Matches 12; Conservative 5; Mismatches
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Cipace: A cut. 1979 Nortis, S.J.; Weinstock, G.W.; White, O.; Sutton, G.G.; Dodson, R.; (Fraser, C.M.; Norris, S.J.; Weinstock, G.W.; White, O.; Sutton, G.G.; Dodson, R.; (Fraser, C.M.; Norris, S.J.; Weinstock, G.W.; White, O.; Sutton, G.G.; Dodson, R.; (Fraser, C.M.; Norris, S.J.; Weinstock, G.W.; White, O.; Sutton, G.G.; Dodson, R.; (Fraser, C.M.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998

A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Reference number: A71250; MUD:9833770; PMID:965876

A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Reference number: A71250; MUD:9833770; PMID:965876

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A; Residues: 1-458 <COL>
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-458 <COL>
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-458 <COL>
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-458 <COL>
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-458 <COL>
A; Status: prosphoprotein C.; Response regulator of the NtrC type; response regulator homology <RRH>
C; Response regulator homology <RRH>
C; Response regulator homology <RRH>
F; 5-114/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 143-355/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymerase sigma factor interaction domain homology <F!>F; 144/Domain: RNA polymera
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C; Species: Vibrio challers
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: D82484
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller; I. R.F.; Medalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUD: 20406833; PMID: 10952301
A; Residues: D8244
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-586 <HEI>A; Residues: 1-586 <HEI>A; Cross-references: GB: AE004364; GB: AE003853; NID: 99657630; PIDN: AAF96157.1; GSPDB:GhA; C; Genetics:
A; Gene: VCA0246
A; Map position: 2
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: C81380
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SgaT protein VCA0246 [imported] - Vibrio cholerae (strain N16961 serogroup
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Pred. No. 30;
8; Mismatches
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5; Mismatches
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25.0%;
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Best Local S
Matches 9
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C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Accession: G97070
R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee,
C; Daty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Residues: 1-243 < KUR>
A; Residues: 1-243 < KUR>
A; Residues: 1-243 < KUR>
A; Cross-references: GB:AE001437; PIDN:AAK79354.1; PID:g15024323; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Genetics:
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status: preliminary
A; Status: preliminary
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Pred. No.
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A; Residues: 1-210 <STO>
A; Cross-references: GB: AE
C; Genetics:
A; Gene: F17L21.2
A; Map position: 1
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Best Local Similarity
Matches 7; Conser
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Matches 10; Conser
                           2 YVFSTEMAN
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43.58;
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Best Local Similarity 43.5
Matches 10; Conservative
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Matches 9; Conser
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A: Residues: 1-662 < PA
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strain C-125
                                                                                                                                                                                          AL139075; GB:AL111168; NID:96967817; PIDN:CAB74209.1; PID:9696784 serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
4317-4331, 2000
me sequence of the alkaliphilic bacterium Bacillus halodurans and
3650; MUID:20512582; PMID:11058132
       quence of the food-borne pathogen Campylobacter jejuni reveals 1250; MUID:20150912; PMID:10688204
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 10-Dec-1999
C; Accession: T01822
R; Edwards, J; Wollam, C.; Dubbelde, C.
Submitted to the EMBL Data Library, August 1998
A; Description: The sequence of A. thaliana T27D20.
A; Reference number: Z14441
A; Accession: T01822
A; Reference number: Z14441
A; Accession: T01822
A; Residues: Lanslated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-319 < EDW>
A; Cross-references: EMBL: AF076274; NID: 93293583; PID: 93377852
A; Experimental source: cultivar Columbia
C; Genetics:
A; Map position: 4
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A; Title: The genome sequence of the food-borne ps A; Reference number: A81250; MUID:20150912; PMID:: A; Accession: C81380
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-311 <PAR>
A; Cross-references: GB:AL139075; GB:AL111168; NII
A; Experimental source: serotype O2, strain NCTC: C; Genetics:
A; Gene: Cj0373
C; Superfamily: phosphoglycerate dehydrogenase
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Pred. No. 18;
6; Mismatches
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Pred. No. 23;
4; Mismatches
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48.0%;
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ilarity 42.4%;
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Best Local Similarity
Matches 14; Conser
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Best Local Similarity
Matches 11; Conser
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te: T27D20.16
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probable bacteriophage protein STY1061 [imported] - Salmonella enterica subsp. enter c; Species: Salmonella enterica subsp. enterica serovar Typhi G; Species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: AD0623 R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc H; Pr.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far Nature 413, 848-852, 2001 A; Muthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s, A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                              Y.; Allard, G.; Awayez, M.J.; C
Peng, X.; Thi-Ngoc, H.P.; Redde
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A; Molecule type: DNA
A; Residues: 1-352 < KUR>
A; Cross-references: GB: AE006641; NID: g13813507; PIDN: AAK40693.1; GSPDB: GN00155
C; Genetics:
A; Gene: pepQ
C; Superfamily: X-Pro aminopeptidase
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A;Cross-references: GB:AL513382; PIDN:CAD05454.1; PID:g16502215; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                             prolidase (Xaa-Pro dipeptidase) (pepQ) [imported] - Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C; Accession: F90179 R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.Farett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Submitted to GenBank, April 2001 A; Description: Sulfolobus solfataricus complete genome.
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
    Gaps
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Pred. No. 35;
3; Mismatches
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Pred. No.
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C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1998
C;Accession: S08500, $31944
A;Title: Molecular organisation of the quinic acid utilization (QUT) gene cluster in Asperatus: preliminary
A;Reference number: S08498; MUID:89181521; PMID:2976880
A;Reference number: S08498; MUID:89181521; PMID:2976880
A;Reference number: S08500
A;Status: preliminary
A;Resions: EmBL.X13525; NID:92398; PID:92399
A;Nolecule type: DNA
A;References: EmBL.X13525; NID:92398; PID:92399
A;Note: the authors translated the codon GCG for residue 327 as Thr
R;Lanb, H.K.; Hawkins, A.R.; Smith, M.; Harvey, I.J.; Brown, J.; Turner, G.; Roberts, C.
Mol. Genet. 223, 17-23, 1990
A;Relerence number: S1944; MUID:91080861; PMID:2175387
A;Residues: 1:326, T' < LAM>A;Reserence number: S1944
A;Molecule type: DNA
A;Residues: 1:326, T' < LAM>A;Residues: 1:326, T' < LAM>A;Reperimental source: strain 2035
C;Genetics:
A;Introns: 57/1; 104/1; 250/2; 293/2
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C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; Accession: C69962
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
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                                                                    A; Description: The sequence of C. elegans cosmid T18H9, A; Reference number: 220666
A; Accession: T29695
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-586 < DUZ>
A; Cross-references: EMBL: U41746; PIDN: AAA83334.1; CESP: T18H9.1
C; Genetics:
A; Gene: CESP: T18H9.1
A; Introns: 23/1; 105/3; 174/3; 303/3; 403/2; 430/3; 539/2
                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                        November 1995
                                                                                                                                                                                                                                                                                                                                                                 Score 46.5; DI
Fred. No. 70;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VYVFSTEMANKAAEAVLKGQVETIVSF
C;Accession: T29695
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VYVESTEMANKAAEAVLK 18
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[larity 40.7%;
Conservative 7,
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RKAGQLLLE
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Best Local Similarity
Matches 11; Conser
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Matches 7; Conser
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13 IYAFATDLA
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y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sc
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy;
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: C69962
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-363 < KUN>
A; Residues: 1-363 < KUN>
A; Cross-references: GB:299116; GB:AL009126; NID:92634723; PIDN:CAB14338.1; PID:926348
A; Experimental source: strain 168
C; Genetics:
A; Genetic
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B95887

probable aminotransferase protein [imported] - Sinorhizobium mellioti (strain 1021) n
C; Species: Sinorhizobium mellioti
C; Date: 24-Aug-2001 *Sequence_revision 24-Aug-2001 *text_change 30-Sep-2001
C; Accession: E95887

R; Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroccession: E95887

R; Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroccession: E95887

A; Fitan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroccession: E95887

A; Fitan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herroccession: E95887

A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Residues: Irelation T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub]
A; Restinental source: strain 1021, megaplasmid pSymB

R; Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub]
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Sclence 293, 668-672, 2001

A; Atthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Iselan, Phebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, R.; Yeh, A; Contents: annotation

C; Genetics: annotation

C; Genetics: Sub.20379

A; Gene Sub.20379
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Pred. No. 65;
4; Mismatches
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5.1.6
Compugen Ltd.
GenCore version
ight (c) 1993 - 2003
             Copyr
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- protein search, using sw model OM protein 2003, 10:27:32; Search time 3.37743 Seconds 15, October Run on:

(without alignments)
389.867 Million cell updates/sec

US-09-915-543-15_COPY_17_204 136 1 VYVFSTEMANKAAEAVLKGOVETIVSFH 28 Title: Perfect score: Sequence:

seqs, 47026705 residues .0.0 , Gapext 0.5 BLOSUM6; Gapop 1 127863 Scoring table: Searched:

tisfying chosen parameters: Total number of hits sa

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution. Pred. No. is the score greater tha and is derived by

		d¥			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	! !
m	13	0	1426	Н	BCL9_HUMAN	000512 homo sapien	apien
7	86	72.1		~	BCL9_DROME	Q961d9 drosop	hila
m	09	44.1		Н	HEM2_CLOJO	Q59295 clostridium	idium.
4	51	37.5		Н	SYV_FUGRU		ubrip.
5	46	33.8		~	QUTG_EMENI		ella
9	46	33.8		H	BUK_BACSU		ns sn
7	4	33.8		Н	HFA1_YEAST		ᄄ
ω	ю	33.5			SODM_CHAFE	096347 charybdis	disf
σ	'n	33.5			GUNN_ERWCA		a car
10	45.5	33.5			GUNW_ERWCA	Q59395 erwinia	a car
11	'n	33.5		~	GUNV_ERWCA	erwini	a car
12	رى رى	33.5		Н	ZP2_MACRA	macaca	radi
13	45	33.1		Н	PEM3_ARATH		lopsis
14	44.5	32.7		Н	AIG2_ARATH		lopsis
15	44		318	Н	YB64_METJA		22020
16	44	32.4	340		MPCP_CAEEL	P40614 caenorhabdi	habdi
17	44	32.4	484		SGAT_ECOLI	P39301 escherichi	ichia
18	44	•	602		DNLI_AERPE	Q9yd18 aeropyrum	rum p
19	44	32.4			SYR_PYRFU		snoo
20	44	32.4			SYV_SCHPO		sacch
21	44	32.4			PKSL_BACSU	Q05470 bacillus	ns sn
22	43	31.6			THI2_CAEEL	Q17424 caenorhabdi	habdi
23	43	31.6			RIB4_SCHPO		sacch
24	43	31.6			EX53_MYCPN		asma
25	43	31,6			TRPD_SULTO	_	snqo.
26	43	31,6			AREH_SCHPO		sacch
27	43	31.6			YDGE_SCHPO	Q10499 schizosacch	sacch
28	43	31.6			SYV_RAT	004462 rattus	norv
29	43	31.6			GLSL_HUMAN	2 homo	sapien
30	43	31.6			NPRV_VIBPR	l vibr	prot
31	43	31.6	611	Н	EMPA_VIBAN	_	angn
32	43	31.6			VGLF_CDVO	<u>_</u>	dist
33	43	31.6			SECA_CYACA	Ξ	lium c

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CAUTION: It is uncertain whether Met-1 or Met-27 is the initiator. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 1391.

Q15269 homo sapien P30733 solanum tub	Q9z1q9 mus musculu P26640 homo sapien	P28367 bacillus su	P93407 oryza sativ	Q8ty76 methanopyru	P70955 bacillus su	Q57672 methanococc	Q9vhq7 drosophila	067887 aquifex aeo	094065 candida alb
PWP2_HUMAN PHYA_SOLTU	SYV2_MOUSE SYV2_HUMAN	RF2_BACSU	SODP_ORYSA	AROD_METKA	YCCH_BACSU	VATC_METJA	O85B_DROME	UVRC_AQUAE	MSH4_CANAL
7	ΗН	Н,		~		Н	Н	Н	Н
919	1263 1264	366	7.11	215	233	381	390	266	803
9.9	31.6	4	، ند	o.	6.	٥.	6.	6	o.
31	31	31	0 9	30	30	30	30	30	30
4 3	44 44 W W	42.5	7.7	42	42	42	42	42	42
3.4 3.5	36 37	38	χ) . Σ) (40	41	42	43	44	45

ALIGNMENTS

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MEDLINE-21952490; PubMed=11955446;

Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.;

Murone M., Zuellig S., Basler K.;

"Wnt/wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";

Cell 109:47-60(2002).

-!- FUNCTION: Involved in signal transduction through the wnt pathway.

-!- FUNCTION: Involved in signal transduction through the wnt pathway.

-!- SUBGELLULAR LOCATION: Nuclear (Probable).

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- TISSUE SPECIFICITY: Detected at low levels in thymus, prostate, testis, ovary and small intestine, and at lower levels in spleen, colon and blood.

-!- DISEASE: Involved in a t(1;14)(q21;q32) chromosomal translocation found in a patient with precusor B-cell acute lymphoblastic leukemia (ALL). This translocation leaves the coding region intact, but may have pathogenic effects due to alterations in the expression level of BCL9. Several cases of translocations within the malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Fetal brain;
MEDLINE=98158621; PubMed=9490669;
Willis T.G., Zalcberg I.R., Coignet L.J.A., Wlodarska I., Stul M.,
Jadayel D.M., Bastard C., Treleaven J.G., Catovsky D., Silva M.L.M.,
Dyer M.J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a novel
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of translocation t(1;14)(q21;q32) defines gene (BCL9) at chromosome 1q21.";
Blood 91:1873-1881(1998).
                                                                     000512;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
B-cell lymphoma 9 protein (Bcl-9) (Legless homolog).
                                                PRT; 1426 AA
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                          BCL9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION.
BCL9_HUMAN

ID BCL9_HU
AC 000512;
DT 28+FEB
DT 28+FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 15-SEP.
OS HOMO S
OC MAMMALIN

RA WILLIS

RA MULCH

CC EUS ECC

-1-SU

CC -1-SU

CC -1-FU

CC -1-FU

CC -1-CA

CC -1-CA
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HEM2_CLOJO
Q59295;
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HEM2_CLOJO
                  REATER-BEATKALE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDIANE-20196006; PubMed-10731132;

REDIANE-20196006; PubMed-10731132;

REDIANE-20196006; PubMed-10731132;

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Zandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Roders Y. T.-H.C., Blazei R.G., Change M., Pfeiffer B.D.,

RA Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Baxa A., Baxendale J., Baytarkaroglu L., Beasley E.M.,

Beson K.Y., Benos P.V., Bernan B.P., Bhandarl D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Bratkarroglu L., Beasley E.M.,

Beson K.Y., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Borlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Plukov B.C.,

Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Plukov J.,

Brables B., Gorrell J.H., Gu Z., Guan P., Harris M.,

Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,

Alarey D., Helman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Ketchum K.A.,

Jalali M., Kallush F., Karpen G.H., Ket Z., Kennison J.A., Ketchum K.A.,

Jalali M., Mallush R.W., Mowland T.J., Wall M., Illang Y., Lin X.,

Martiel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., Wolntosh T.C., McLeod M.P., Marny D.M., Nebsen D.L.,

Mount S.M., Moy M., Murphy B., Murphy L., Muary D.M., Nebsen M.G.,

Ral Bazzolo M., Pittman G.S., Pan S., Pollard J., Mosher E., Shen H.,

Spier E., Spradling A.C., Stapleton M., Strong R., Poller E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X.,

Wang Z.Y., Wang A.M., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D BCL9_DROME STANDARD; PRT; 1469 AA.

Q961D9; Q9V4D2;
T 28-FEB-2003 (Rel. 41, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 42, Last annotation update)
T 15-SEP-2003 (Rel. 42, Last sequence update)
T 15-SEP-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, L
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                                                                                                                      hromosomal translocation; Proto-oncogene;
                                                                                                                                                                                                                                                                                           POLY-ALA.
POLY-PRO 3.
W; A240A487716B7F1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 136; DB 1;
Pred. No. 3.1e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VYVFSTEMANKAAEAVLKGOVETIVSFH 204
                                                                                                                                                                                                                                       POLY-PRO 1.
POLY-PRO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKAAEAVLKGQVETIVSFH 28
         3942.1; ALT_FRAME. BCL9.
                                                                                               oncogenesis; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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Best Local Similarity 100.
Matches 28; Conservative
EMBL, Y13620; CAA73942.1
Genew; HGNC:1008; BCL9.
MIM; 602597; -.
GO; GO:0007048; P:oncoge
Nuclear protein; Chromos
Wnt signaling pathway.
DOMAIN 347 377
DOMAIN 347 377
DOMAIN 331 335
DOMAIN 331 335
DOMAIN 970 903
SEQUENCE 1426 AA; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYVESTEMA
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BCL9_DROME
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AY051651; AAR93075.1; -.
EMBL; AF457205; AAL91368.1; -.
EMBL; AF457205; AAL91368.1; -.
FlyBase; FBgn0039907; 1gs.
GO; GO:0005634; C:nucleus; IEP.
GO; GO:0030177; P:positive regulation of Wnt receptor signali. . .; IPI.
GO; GO:0003177; P:segment polarity determination; IMP.
Nuclear protein; Developmental protein; Segmentation polarity protein;
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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MEDLINE-21952490; PubMed=11955446;

Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.;

"Wnt/wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";

Cell 109:47-60(2002).

-!- FUNCTION: Involved in signal transduction through the wnt pathway.
-!- SUBGELUIAR LOCATION: Nuclear.
-!- SUBCELUIAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically
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ASN-RICH.
GLN-RICH.
POLY-ASN.
G->E: IN ALLELE LGS-21L.
L->F: IN ALLELE LGS-17E; SEGMENT POLARITY PHENOTYPE.
                                                                                                                                                                                                                                                                                                                               ., Wan K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE OF 6-1469 FROM N.A., AND MUTAGENESIS OF GLY-514; LEU-534 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  throughout development.
-!- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
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                                                                                                                                                                                                                        STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S.
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
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Pred, No. 1.6e-06;
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W; 5672E01B7200ED08 CRC64;
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Best Local Similarity 57.1%;
Matches 16; Conservative 9
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1449
1169
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1469 AA;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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P25416;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (Porphobilinogen synthase) (ALADH) (Fragment).
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VARS1.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Takifugu,
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FERM P-9684;
MEDLINE=95394829; PubMed=7665501;
Fujino E., Fujino T., Karita S., Sakka K., Ohmiya K.;
"Cloning and sequencing of some genes responsible for porphyrin blosynthesis from the anaerobic bacterium Clostridium josui.";
J. Bacteriol. 177:5169-5175(1995).
-:- CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen +
                                                                                                                                                                                                                        es; Clostridia; Clostridiales; Clostridiaceae;
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Probom: PD002304; Alab_dehydratase; 1.
PROSITE; PS00169; D_ALA_DEHYDRATASE; PARTIAL.
Porphyrin biosynthesis; Lyase; Zinc.
DOMAIN 114 132 ZINC-BINDING (BY SIMILARITY).
NON_TER 205 205
SEQUENCE 205 AA; 23172 MW; 886F9DAEFDB1144E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23172 MW; 886F9DAEFDB1144E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H(2)O.
-1- COFACTOR: Zinc (By similarity).
-1- PATHWAY: Siroheme biosynthesis.
-1- SUBUNIT: Homooctamer (By similarity).
-1- SIMILARITY: BELONGS TO THE ALADH FAMILY.
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PIR; I40812; I40812.
HSSP; P15002; 1B4E.
InterPro; IPR001731; Alab_dehydratase.
Pfam; PF00490; ALAD; 1.
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Best Local Similarity
"-hes 12; Conserv
                                                                                                                                                                                     Clostridium josui.
Bacteria, Firmicut
Clostridium.
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YHFSPDMVG
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                                                                                                                             synthase) (ALAD)
HEMB.
                                                                                                                                                                                                                                                              CLUSCIIGIUM.
NCBI_TaxID=1499;
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P49696;
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SYV_FUGRU
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DR InterPro; IPR001412; tRNA-synt_la.

DR InterPro; IPR001412; tRNA-synt_la.

DR Pfam; PF00133; tRNA-synt_la.

DR Pfam; PF00130; tRNA-synt_la.

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                                                                                                                                                                                                                                      + diphosphate
Lim E.H., Corrochano L.M., Elgar G., Brenner S.;
"Genomic structure and sequence analysis of the valy1-tRNA synthetase gene of the Japanese pufferfish, Fugu rubripes.";
DNA Seq. 7:141-151(1997).
-!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valy1-tRNA(Val).
-!- SIMILARITY: Belongs to class-I aminoacy1-tRNA synthetase family.
-!- SIMILARITY: THE N-TERMINAL DOMAIN IS SIMILAR TO ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91080861; PubMed=2175387;
Lamb H.K., Hawkins A.R., Smith M., Harvey I.J., Brown J., Turner G.,
Roberts C.F.;
"Spatial and biological characterisation of the complete quinic acid
utilisation gene cluster in Aspergillus nidulans.";
Mol. Gen. Genet. 223:17-23(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89181521; PubMed-2976880; Hawkins A.R., Lamb H.K., Smith M., Keyte J.W., Roberts C.F.; "Molecular organisation of the quinic acid utilization (QUT) gene cluster in Aspergillus nidulans."; Mol. Gen. Genet. 214:224-231(1988).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
NCBL_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
QUTG protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR 1-GAMMA.
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HFA1_YEAST
P32874;
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A Acedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Devedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Chiz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Chiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many sporulation genes.";
Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34, Created)
34, Last sequence update)
41, Last annotation update)
kinase (EC 2.7.2.7) (BK) (Branched-chain carboxylic
FUNCTION: NOT KNOWN. PROBABLY INVOLVED IN QUINATE METABOLISM.
SIMILARITY: Belongs to the inositol monophosphatase family.
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                           33.8%; Score 46; DB 1; Length 330; 38.9%; Pred. No. 21; 1ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                   36762 MW; 11CD80C65E077A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AA
                                                                                                                                     EMBL; X13525; CAA31878.1; ALT_SEQ. PIR; S08500; S08500.
HSSP; P29218; 11MF.
InterPro; IPR000760; Inositol_P. Pfam; PF00459; inositol_P; 1.
ProDom; PD023420; Inositol_P; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8969508;
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IYAFATDLARKAĞQLILE 30
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                              IMP
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=97124195; Pt
Mizuno M., Masuda S.
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P54532;
01-0CT-1996 (Rel. 3
01-0CT-1996 (Rel. 3
28-FEB-2003 (Rel. 4
Probable butyrate k
                                                                                                                                                                                                                         PROSITE; PS00629; II
PROSITE; PS00630; II
Quinate metabolism.
SEQUENCE 330 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid kinase).
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Bacillus
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BUK_BACSU
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Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
Subtilis.",
Subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: ATP + 2-butanoate = ADP + butanoyl phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 23;
1; Mismatches 3; Indels
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HFAI protein.
HFAI OR YMR207C OR YM8261.01C OR YM8325.08C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01075; ACETATE_KINASE_1; 1. PROSITE; PS01076; ACETATE_KINASE_2; 1. Transferase; Kinase; Complete proteome SEQUENCE 363 AA; 39764 MW; 94ADA51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; C69962; C69962.
SubtiList; BG11724; buk.
HAMAP; MF_00542; -; 1.
InterPro; IPR000890; Acetate_kin.
Pfam; PF00871; Acetate_kinase; 1.
PRINTS; PR00471; ACETATEKNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%;
71.4%;
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293 AASAALKGEVEAIV 306
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Best Local Similarity 71.4°
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STRAIN=S288c / AB972;
PubMed=9169872;
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GUNN_ERWCA
Q59394;
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METAL
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                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                             SIMILARITY: STRONG, TO ACETYL-COA CARBOXYLASE.
CAUTION: THE READING FRAME FROM WHICH THIS PROTEIN IN TRANSLATED HAS NO MET INITIATION CODON NEAR TO THE 5'END. IT DOES NOT SEEM TO BE A PSEUDOGENE. THERE ARE NO APPARENT FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                    cerevisiae gene closely related
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
Charybdis feriatus (Crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Charybdis.
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Pred. No. 1.5e+02;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BIOTIN (BY SIMILARITY).
F -> L (IN REF. 2).
W; 08727A301549DA92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_carb_C.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000022; Carboxyl_trans.
InterPro; IPR000249; Carboxyl_trans.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_D1.
IPR03184; Biotin_lipoyl; 1.
IPR0317E; PS00188; BIOTIN; 1.
IPR0517E; PS00188; BIOTIN; (BY SACT_SITE A59 BY SIMILA BINDING 804 BOTIN (BSCONFLICT 661 F-> L(I
                                                                                                                    s (acetyl-CoA carboxylase).";
Seq. 4:69-70(1993).
COFACTOR: BIOTIN (BY SIMILARITY).
SIMILARITY: STRONG, TO ACETYL-COA
CAUTION: THE READING FRAME FROM WH
                                                                                                  a Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PubMed=7906156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z49809; CAA89922.1; -.
EMBL; Z48755; CAA88647.1; -.
EMBL; Z22558; CAA80280.1; -.
PIR; S55089; S55089.
HSSP; P24182; 1DV1.
SGD; S0004820; HFA1.
InterPro; IPR001882; Biotin_at InterPro; IPR005482; Biotin_cat InterPro; IPR00089; Biotin_li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
ilarity 45.0%;
Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDARD;
1997).
                                   SEQUENCE OF 125-94
MEDLINE=94146412; I
Kearsey S.E.;
"Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVFSTEMA
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SEQUENCE FROM N
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SODM_CHAFE
ID SODM_CHAFE
AC 096347;
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Best Local S
Matches 9
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Qγ
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                                                                                                                                    the
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MEDLINE=9829944; PubMed=9636315;
Olsen O., Thomsen K.K., Weber J., Duus J.O., Svendsen I., Wegener C., yon Wettstein D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Biotechnology 14:71-76(1996).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
Lin C.T., Lai Y.S., Kuo T.J., Chang T.C.;
"Molecular cloning, expression, and characterization of a cDNA encoding Mn-superoxide dismutase from crab Charybdis feriatus.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Destroys radicals which are normally produced within tells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Manganese (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase N precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION (BY SIMILARITY).
SUPEROXIDE DISMUTASE [MN].
MANGANESE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019411; AAD01640.1; -.
HSSP; P04179; 1ABM.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
Pfam; PF02777; sodfe_C; 1.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD_MN; 1.
Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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5
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 YVFSTEMA-NKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 YVNNLNVAEEKLAEAKEKGDVSTIIS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred
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94 MZ
177 MZ
181 MZ
24527 MW;
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Local Similarity 50.0%;
Nes 13; Conservative
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46
94
177
181
224 AA;
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GUNV_ERWCA
Q47096;
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ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                         CHAIN
DOMAIN
DOMAIN
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                g
                                                            ntry is copyright. It is produced through a collaboration s Institute of Bioinformatics and the EMBL outstation - nformatics Institute. There are no restrictions on its it institutions as long as its content is in no way statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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35, Last sequence update)
41, Last annotation update)
precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95231512; PubMed-7715600;
Mae A., Heikinheimo R., Palva E.T.;
"Structure and regulation of the Erwinia carotovora subspecies carotovora SCC3193 cellulase gene celv1 and the role of cellulase in phytopathogenicity.";
Mol. Gen. Genet. 247:17-26(1995).
-:- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoglucanase VI precursor (EC 3.2.1.4) (Endo-1,4-beta-giucamase (Cellulase VI).
CELVI.
Erwinia carotovora.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pectobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
FA7E4179004CBB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                   A3H.
)1956; CBD_3.
)1547; Glyco_hydro_5.
CBM_3; 1.
cellulase; 1.
347; CBD_3; 1.
559; GLYCOSYL_HYDROL_F5; 1.
fadation; Hydrolase; Glycosidase; Signal.
POTENTIAL.
POTENTIAL.
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NKVKEAVAAAQSLGVYIIIDWH 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48300 MW;
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ilarity 36.7%;
Conservative
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168
256
                                                                                            between the Swiss
the European Bioinf
use by non-profit
modified and this s
entities requires a
                                                                                                                                                                                                                                                                                                     EMBL; L39788; AAC37
HSSP; 085465; 1A3H.
InterPro; IPR001956
InterPro; IPR001547
Pfam; PF00942; CBM.
Pfam; PF00150; cell
ProDom; PD001947; CPNOSTE; PS00659; Cellulose degradatiscellulose degradatiscellulose agradatiscellulose agradatiscellulo
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nes 11; Conser
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YISNPSLAN
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MEDLINE-95231512;
                                                               This SWISS-PROT
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S54744; S
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SEQUENCE
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Q59395;
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PIR; S
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GUNW_ERWCA
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Matches
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SETTITION OF STATE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-!- FUNCTION: Endoglucanase with some exoglucanase activity.
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: Has a pH optimum of about 7.0 and a temperature optimum about 42 degrees Celsius.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
(Cellulase V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme
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Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                            CATALYTIC.
LINKER.
CELLULOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
OD7ECF74781565FA CRC64;
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MEDLINE=94067016; PubMed=8246888;
Cooper V.J.C., Salmond G.P.C.;
"Molecular analysis of the major cellulase (CelV) of Erwinia carotovora: evidence for an evolutionary 'mix-and-match' of edomains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
HSSP; O85465; 1A3H.
InterPro; IPR001956; CBD_3.
InterPro; IPR001547; Glyco_hydro_5.
Pfam; PF00942; CBM_3; 1.
Pfam; PF00150; cellulase; 1.
ProDom; PD001947; CBD_3; 1.
ProDom; PS00659; GLYCOSYL_HYDROL_F5; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                                                                                                                          ENDOGLUCANASE V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45.5; Di
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101 YIANPSLANKVKEAVAAAQGLGVYIIIDWH 130
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5; Mismatches
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                                                                                                                                                                                                                                                                     POTENTIAL
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HSSP; O85465; 1A3H.
InterPro; IPR001956; CBD_3.
InterPro; IPR001547; Glyco_hydro_5.
Pfam; PF00942; CBM_3; 1.
Pfam; PF00150; cellulase; 1.
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334
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504
168
256
NA
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ilarity 36.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                              32
32
335
353
168
256
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nes 11; Conserv
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                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50:229-239(1998).
FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA, IN ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1. SECONDARY SPERM RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca radiata (Bonnet monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                   38, Created)
38, Last sequence update)
39, Last annotation update)
erm-binding protein 2 precursor (Zona pellucida (Zona pellucida protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION: Type I membrane protein. Extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY AN E IN THE POSTFERTILIZATION BLOCK TO POLYSPERMY. GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00682; ZP_DOMAIN; 1.
Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
Extracellular matrix.
                                                                                               CELLUIOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
DBEA9337BB4D2623 CRC64;
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                                                                                                                                                                     505;
                                                                                                                                                                                                   Indels
                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; PubMed=9590540;
, Santhanam R., Gupta S.K.;
ing and expression in Escherichia coli o
monkey (Macaca radiata) zona pellucida
                               Signal
                                                                                                                                                                     DB 1;
                             Hydrolase; Glycosidase;
POTENTIAL.
                                                        ENDOGLUCANASE V. CATALYTIC.
                                                                                                                                                                    Score 45.5; Dl
Pred. No. 38;
5; Mismatches
                                                                                                                                                                                                                                             101 YISNPSLANKVKEAVAAAQSLGVXIIIDWH 130
                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                           KAAEAVLKGQ---VETIVSFH 28
                                                                                                                                                                                                                                                                                                                          745
  CBD_3; 1.
GLYCOSYL_HYDROL_F5; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT ROLE IN THE POSTFERTILI.
PTM: SULFATED GLYCOPROTEIN WITH O
(BY SIMILARITY).
SIMILARITY: Contains 1 ZP domain.
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                                                                                     LINKER
                                                                                                                                                                                                                                                                                                                          PRT;
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3; ZPELLUCIDA.
                                           31 PC
505 B3
334 C2
352 L.
505 C1
168 P1
256 NN
                                                                                                                                                                    33.5%;
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Prodom; PD001947; C
PROSITE; PS00559; G
Cellulose degradati.
SIGNAL 1
CHAIN 32
DOMAIN 32
DOMAIN 335
ACT_SITE 168
ACT_SITE 256
SEQUENCE 505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding bonnet mon
glycoprotein-ZP2.";
Mol. Reprod. Dev. 5
-!- FUNCTION: ZP2 F
WHICH ZP2 AND Z
ZP2 ACTS AS A S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Ovary;
MEDLINE=98250422; F
Jethanandani P., Sa
"Molecular cloning
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix.
PTM: IS PROTEC MODIFICATION,
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PRINTS; PR00023;
                                                                                                                                                                                                                                                                                                                                                                                           zona pellucida spe
glycoprotein ZP2)
ZP2.
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                                                                                                                                                                                                                          2 YVFSTEMA
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15-JUL-1999
30-MAY-2000
                                                                                                                                                                                                                                                                                                                         ZP2_MACRA
077726;
                                                                                                                                                                                                                                                                                              RESULT 12
ZP2_MACRA
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO N.A.

MEDLINE-21016719; PubMed=11130712;

A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

A Chung M.K., Conn L., Fong J.-D., Fong B., Fujii C.Y.,

A Chung M.K., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

A Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished observations (MAY-2002).
-!- FUNCTION: Catalyzes N-methylation of phosphoethanolamine, the phosphomonomethylethanolamine and phosphodimethylethanolamine to three methylation steps required to convert phosphoethanolamine to phosphocholine (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + ethanolamine phosphate = S-adenosyl-L-homocysteine + N-methylethanolamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER3_ARATH STANDARD; PRT; 490 AA.

29-C6B9; Q9C9V1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Putative phosphoethanolamine N-methyltransferase 3 (EC 2.1.1.103).

NMT3 OR ATIG73600 OR F6D5.1 OR F25P22.1.

Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                           ď
                         ZONA PELLUCIDA SPERM-BINDING PROTEIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                             (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                    .
О
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 745;
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                                                                                                                                            N-LINKED (GLCNAC. . .) (POT N-
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                          POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYVFSTEMA-----NKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 57;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Score 45.5;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                            82710 MW;
                                                                                                                                                                                                                                                                                                                                                                         33.5%;
nilarity 29.7%;
Conservative 6
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38
745
716
736
736
637
637
105
122
223
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          745 AA;
   39
39
39
370
370
105
122
223
310
400
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                                                                      TRANSMEM
DOMAIN
DOMAIN
CARBOHYD
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
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                                                                                                                                                                                                   CARBOHYD
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                       CHAIN
DOMAIN
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PEM3_ARATH
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jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reuber T.L., Ausubel F.M.; "Isolation of Arabidopsis genes that differentiate between resistance responses mediated by the RPS2 and RPM1 disease resistance genes."; Plant Cell 8:241-249(1996).
BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
[.1 (AAG51806) sequence differs from that shown due to
ene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIG2 protein.

AIG2 OR AT3G28930 OR K5K13.3 OR K5K13.1.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                   Length 490;
                                                                                                                                                                                                                             SAM-BÎNDING 1.
SAM-BINDING 2.
77FDFAFBC89C41CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4C4F6417143AE30 CRC64;
                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34, Created)
34, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                                                                                                                  Score 45; DB
Pred. No. 44;
                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                 Transferase; Methyltransferase; Repeat
                                                                                                                                                           EMBL; AC079676; AAG51806.1; ALT_SEQ. EMBL; AC012679; AAG52075.1; ... InterPro; IPR001601; Methyltransf. InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                       FSTEMANKAAEAVLKGQVETIV 25 | : | | : | : : : : : FTTELAQKAGQVIAVDFIESVI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-96351417; PubMed-8742710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAA95744.1; -
                                                                                                                                                                                                                                                         56368 MW;
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y 31.8%;
rvative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U40857; AAC49283.1;
EMBL; AB025615; BAA95744.1
SEQUENCE 170 AA; 19445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clones.";
DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
SIMILARITY: BEL
CAUTION: Ref.1
erroneous gene
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 01-OCT-1996 (Rel. 28-FEB-2003 (Rel.
                                                                                                                                                                                                                               49
278
490 7
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P54121;
                                                                                                                                                                                                                             DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AIG2_ARATH
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collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=9637999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Button G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE PBSX(XRE) FAMILY OF TRANSCRIPTIONAL REGULATORS. ARCHAEAL 1 SUBFAMILY.
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Hypothetical protein; Transcription regulation; DNA-binding;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical transcriptional regulatory protein MJ1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 171 H-T-H MOTIF (POTENTIAL).
318 AA; 36529 MW; F7E61B67F09263CD CRC64;
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      DB 1;
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Pred. No. 40;
5; Mismatches
                                                                                                                                                                                                                                                                                                                        318 AA
                               Pred. No. 18;
0; Mismatches
    Score 44.5;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 15, 2003, 10:31:00
                                                                                                                  6 TEMANKAAEAVL----KGQVETIV
                                                                                                                                                                         85 TEYVRKTVEVVLTDTLEKKOVETIV
                                                                                                                                                                                                                                                                                                                      PRT;
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156 IYKYETQMANPSVDVALK 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67558; AAB99166.1; -. PIR; C64445; C64445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.4%;
38.9%;
Query Match 32.7%;
Best Local Similarity 52.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00584; -; 1.
InterPro; IPR001387; HTH_3.
Pfam; PF01381; HTH_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2190;
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15, 2003, 10:27:33 ; Search time 16.2335 Seconds (without alignments) 445.097 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                      US-09-915-543-15_COPY_177_204
136
1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                            seqs, 258052604 residues
                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 protein search, using sw model
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_hage:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	Q9u1q4 caenorhabdi	Q97ja0 clostridium	Q9v611 drosophila	Q960e6 drosophila	O82521 capsicum ch	Q9h6r2 homo sapien	Q96gn2 homo sapien	Q96q02 homo sapien	Q8ggi9 lactobacill	Q91fw7 arabidopsis	Q976c9 sulfolobus	Q8g3s3 bifidobacte		Q96ya9 sulfolobus	Q96x55 sulfolobus	Q8dfx2 vibrio vuln
SUMMARIES	ID	Q9U1Q4	Q97JA0	Q9V6L1	0960E6	082521	Q9H6R2	Q96GN2	096002	086619	Q9LFW7	629760	08G3S3	Q9FZL1	096 YA9	096 X 55	Q8DFX2
	DB		16	Ŋ	Ŋ	10	4	4	4	7	10	17	16	10	17	17	16
	Length DB	1050	243	1049	1049	459	642	642	1098	350	141	143	187	210	233	237	268
	% Query Match	40.4	37.5	37.5	37.5	36.8	36.8	36.8	36.8	36.4	36.0	36.0	36.0	36.0	36.0	36.0	36.0
	Score	55	51	51	51	50	20	20	20	49.5	49	49	49	49	64	49	49
	Result	H	7	m	₹	ហ	9	7	æ	0	10	11	12	13	14	15	16

083532 treponema p Q9kms4 vibrio chol Q8tfz1 aspergillus Q9pic9 campylobact	096497 trypanosoma Q96z50 sulfolobus Q97697 sulfolobus	Q9K/94 bacillus na Q91v35 arabidopsis Q8bin9 mus musculu	Q9y7e9 candida gla Q8iwq9 homo sapien	Q8xkx> clostrigium Q8gj63 bartonella		Q8pinO streptococc Q8rvv4 lycopersico O92203 mus musculu	08z743 mus muscus 08z743 salmonella 08eai4 shewanella	ŋ		Q8efd3 shewanella	Q22551 caenorhabdi O19380 caenorhabdi	
16 083532 16 Q9KMS4 3 Q8TFZ1 16 Q9PIC9	0.096497 17 096250 17 0976P7		$\alpha \alpha$	10 Q8GJ63		10 Q8RVV4 11 092203		3 Q8WZX5 5 Q8MMT3	ď	16 Q8EFD3	5 Q22551 5 Q19380	S QBLJX6
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ALIGNMENTS

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Y87G2A.5 protein.
Y87G2A.5.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

Science 282:2012-2018(1998).

Rembl, AL110500; CAB60428.1; -.

RHSSP; P96142; 1GAX.

RHSSP; P96142; 1GAX.

ROTHPEP: Y87G2A.5; CE24685.

InterPro; IPR002300; tRNA-synt_1a.

InterPro; IPR001412; tRNA-synt_1.

R InterPro; IPR00130; tRNA-synt_1.

R Pfam; PF00133; tRNA-synt_1; 1.

R Pfam; PF00133; tRNA-synt_1; 1.

R Pfam; PF00134; ANA-SYNT_1; 1.

R PROSITE; P800178; AA_TRNA_LIGASE_1; 1.

R PROSITE; P800178; AA_TRNA_LIGASE_1; 1.
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                                                                                       PRT; 1050 AA
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MEDLINE=99069613; PubMed=9851916;
                                                                                       PRELIMINARY;
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                                                                                    Q9U1Q4
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubols J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007650; AAK79354.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
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rygota; Diptera; Brachycera; Muscomorpha;
ophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 16; Length 243; Pred. No. 18;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG4062 protein.
AATS-VAL OR CG4062.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pte
Neoptera; Endopterygota; Diptera; Brachycera; Muscomori
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Zn-dependent hydrolases, glyoxylase family.
CAC1386.
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                                                                       KAAEAVLKGQVETIVSFH
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26880 MW;
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25.0%;
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                              2 YVFSTEMAN
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Matches
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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., A de Pablos B., Dahlke C., Davenport L.B., Davies P., Debrita B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W., A Glodek A., Gong F., Gorrell J.H., Guz., Guan P., Harris M., Howland T.J., Hernandez J.R., Houck J., A Harris M., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Roman B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kuplerson D., A Markilov G., Milshina N.V., Mobarry C., Morles D.M., Nelson D.L., Relact D.R., Nelson K.A., Nixon K., Nusskern D.R., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Relact K., Remington K., Sunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kiamos I., Simpson M., Strong R., Suith T., She Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinston M., Zhou K., Zhu S., Zhon F., Zaveri J.S., Zhan M., Zhou S., Zha G., Zhao Q., Zhao Q., Zhao Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C., Reince 287:2185-2195(2000).
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Redniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Rounnenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome.";
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003819; AAM68598.1; -.
HSSP; P96142; 1GAX.
FlyBase; FBgn0027079; Aats-val.
InterPro; IPR002300; tRNA-synt_1.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002303; tRNA-synt_1.
Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00986; TRNASYNTHVAL.
R TIGRFAMS; TIGR00422; valS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker
Submitted (MAR-2000)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                              Query Match
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Q9H6R2
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STRAIN=habanero;
Aluru M., Curry J., O'Connell M.;
"Nucleotide Sequence of a Probable Aminotransferase Gene (Accession No. AF085149) from Habanero Chile. (PGR98-182).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              082521;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative aminotransferase.
Capsicum chinense.
Capsicum chinense.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     Og60E6 PRELIMINARY; PRT; 1049 AA.

Cg60E6; Og60E6
T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
N AATS-VAL OR CG4062.
S Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

X NCBL_TaxID=7227;
N 013
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                                                           Score 51; DB 5; Length 1049;
Pred. No. 89;
5; Mismatches 11; Indels
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PS00178; AA_TRNA_LIGASE_I; 1.
1049 AA; 118331 MW; 56F322C7414EEAC4 CRC64;
AA_TRNA_LIGASE_I; 1.
.; 118253 MW; 13A513ABF69E8EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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                                                                                                                                                     2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
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ASATEAVRSGELKIIPEHH
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InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
Pfam; PF00133; tRNA-synt_val.
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                                                              37.5%;
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                                                                                                         rvative
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YVSCSDMAA
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Best Local Similarity
Matches 11; Conse
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 PS00178
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PROSITE; P
SEQUENCE
PROSITE;
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Matches
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Q960E6
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., A Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okawabata T., Autani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Tanaka T., Nakamura Y., Suzuki T., Sugano S.;
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
L. Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
REBL; AK025618; BAB15191.1; -.
REBL; AK025618; BAB15191.1; -.
RESP; P96142; IGAX.
InterPro; IPR002309; tRNA-synt_la.
R InterPro; IPR002303; tRNA-synt_la.
R Pfam; PF00133; tRNA-synt_li.
R PRINTS; PR00986; TRNASYNTHVAL.
R PRINTS; PR0986; TRNASYNTHVAL.
R Hypothetical protein.
SEQUENCE 642 AA; 71578 MW; C9E37EEID742B7F1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009355; AAH09355.1; -.
                                                                                                                                                                                                   02ABB4D728B524E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09H6R2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ21965.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                   10;
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51;
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                                                                                                                                                                                                                                                                                                                   4; Mismatches
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Plant Physiol. 118:1102-1102(1998).

EMBL; AF085149; AAC78480.1; -.

HSSP; P04181; 20AT.

InterPro; IPR005814; Aminotrans_3.

Pfam; PF00202; aminotran_3; 1.

PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.

Aminotransferase; Transferase.

SEQUENCE 459 AA; 50729 MW; 02ABB4D728
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                                                                                                                                                                                                                                                         Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            196 FSTRLANNLESLILKEGPETVAAF 219
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Local Similarity 41.7%;
nes 10; Conservative
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Best Local Similarity 44.4
Matches 12; Conservative
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Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                Length 642;
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                                                                                           71650 MW; 1F00CBB73742B579 CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA1885 (Fragment).
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Last sequence update)
Last annotation updat
                                                                                                                            Score 50; DB 4;
Pred. No. 73;
4; Mismatches 1
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                                                                                                                                                                                                                              2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
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AA_TRNA_LIGASE_I; 1
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InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_I.
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00986; TRNASYNTHVAL.
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                    tRNA-synt_val
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002303; tRNA-synt_val
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00986; TRNASYNTHVAL.
Hypothetical protein.
SEQUENCE 642 AA; 71650 MW; 1F0
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                                                                                                                             Query Match 36.8%;
Best Local Similarity 44.4%;
Matches 12; Conservative
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PROSITE; PS00178; AA_T
Hypothetical protein.
NON_TER 1 1
SEQUENCE 1098 AA; 1
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MEDLINE=21456161; Pu
Nagase T., Kikuno R.
"Prediction of the o
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Best Local Similarity
Matches 12; Conser
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Lactobacillus.
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Lactobacillus
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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TISSUE=Br
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Q96Q02;
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Q96Q02
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Q8GGI9
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SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Bringel E., Hubert J.-C.;
Bringel E., Hubert J.-C.;
"Investigation of arginine requirement in Lactobacillus isolated from different environments revealed point mutations, insertions and deletions in arginine blosynthetic genes.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF514870; AAO15990.1; ..
SEQUENCE 350 AA; 38178 MW; 64D1986ED73C8AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence for Arabidopsis thaliana BAC T7N9 from chromosome
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                                                                                                                                                                                                                                                                                                                2; Length 350;
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                          Match 36.4%; Score 49.5; I Local Similarity 54.5%; Pred. No. 45; les 12; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||:: ||||: |
176 VYSTDLLAKAAE---KGQVDAI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VFSTEMANKAAEAVLKGQVETI 24
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Submitted (APR-1997)
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Submitted (JUN-1997)
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01-MAR-2001
01-MAR-2001
01-OCT-2001
F17L21.2.
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STRAIN=JCM 10545 / 7;

Pubbmed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Noshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Noshizawa T., Kikuchi H.;

Oshima T., Kikuchi H.;

"Complete genome sequence of an aerobic thermoacidophilic
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                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                           0976C9 PRELIMINARY; PRT; 143 AA.
0976C9;
01-DEC-2001 (TremBirel. 19, Created)
01-DEC-2001 (TremBirel. 19, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
Hypothetical protein ST0252.
ST0252.
Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
NCBI_TaxID=111955;
M., Vaysberg M., Yu G., Davis R., Federspiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08G3S3 PRELIMINARY; PRT; 187 AA.
08G3S3;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypoxanthine-guanine phosphoribosyltransferase.
HPRT OR BL1681.
Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
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                                                                                                                         Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of an aerobic thermoacidophilic folobus tokodaii strain7.";
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I M.-C., Desiere F., Bork P., Delley M.,
                                                                                                                                                                Indels
                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Complete proteome.
16822 MW; DIAFCC5157298CA2 CRC64;
                                                                                 CRC64;
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43.3%; Pred. No. 20;
iive 4; Mismatches 11;
                                                                                 6FEC48B07326B313
                                                                                                                      Score 49; DB 10;
Pred. No. 19;
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                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                              ADRLAKGELENNVTF 135
                                                                                                                                                                                                        AAEAVLKGQVETIVSF 27
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                                                                                   16649 MW;
                                                                                                                       36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8:123-140(2001).
EMBL; AP000982; BAB65218.1;
Hypothetical protein; Comple
SEQUENCE 143 AA; 16822 MW
Thaveri A., Toriumi M., Vays
Theologis A., Ecker J.;
Submitted (SEP-2000) to the
EMBL; AC000348; AAF79866.1;
SEQUENCE 141 AA; 16649 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 43.3
Matches 13; Conservative
                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 10; Conser
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Pessi G., Zwahlen
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Q8G3S3
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0996C9
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SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004557; AAF99722.1;
InterPro; IPR003822; PAH.
Pfam: PF02671; PAH.
Pridmore R.D., Arigoni F.; "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014802; AAN25468.1; -. Glycosyltransferase; Transferase; Complete proteome. SEQUENCE 187 AA; 20617 MW; E697C3C127277DB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
idicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                 Length 187;
                                                                                                                                                                                                                                                                                           Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                 DB 16;
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                                                                                                                                                                                                                                                                                                                                                7 EMANKAAE------AVLKGQVETIVSF 27
                                                                                                                                                                                                                                                              Pred. No. 26; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                   Score 49;
Pred. No.
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(TrEMBLrel. 16, 1
(TrEMBLrel. 18, 1
                                                                                                                                                                                                                             Query Match 36.0%;
Best Local Similarity 45.2%;
Matches 14; Conservative
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210 AA; 2
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Submitted (DEC-1998)
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Submitted (AUG-2000)
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Submitted (JUN-1998)
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PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermoacidophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=JCM 10545 / 7;
Pubmed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermoacidophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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aeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ii.
aeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Score 49; DB 10; Length 210;
Pred. No. 30;
6; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cremarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000989; BAB67368.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 233 AA; 27253 MW; 8B9E6FDB60EEE36D CRC64;
                                                                                                                                                                                                                                                                                                            O96XA9 PRELIMINARY; PRT; 233 AA.
096XA9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein ST2259.
ST2259.
Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobus.
Sulfolobus.
NCBI_TaxID=111955;
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096X55;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ST1165.
ST1165 OR ST0857.
Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobus.
NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 17;
Pred. No. 34;
5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                       4 FSTEMANKAAEAVLKGQVETIVSF 27
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39.3%; Pred
5; '
      36.0%;
41.7%;
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Best Local Similarity 39.3
Matches 11; Conservative
                                                               rvative
Query Match
Best Local Similarity
Matches 10; Conser
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Q96X55
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Q96YA9
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Gaps
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                                                                                                                           Length 237;
DNA Res. 8:123-140(2001).

EMBL; AP000985; BAB66201.1; -.

EMBL; AP000984; BAB65870.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 237 AA; 27691 MW; B931759A9980D362 CRC64;
                                                                                                                        9; DB 17;
                                                                                                                        Match 36.0%; Score 49; DB Local Similarity 43.3%; Pred. No. 34; les 13; Conservative 4; Mismatches
                                                                                                                                                                                                           1 VYVFSTEMAN -- KAAEAVLKGQVETIVSFH 28
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Human legless homo
Human BCL9 homolog
Human polypeptide
Mouse beta-catenin
Mouse beta-catenin
Human polypeptide
WASP homolog prote
Amino acid sequenc
                                                                                                                          (without alignments)
258.182 Million cell updates/sec
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2. SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3. SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

4. SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotrople; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378
                                                                                                                                                                                                                                                                              This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (lgs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (lgs) protein homologue lgs/bcl9 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPKAPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK
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                                                                                                                           useful in therapeutic method for treating disorders as cell differentiation or cell proliferation \,
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N-PSDB; AAF88467.
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                                                                                                                                                                                                                            Example II;
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Sequences ABBB10981-ABBB1230 represent 1350 novel human polypeptides, and sequences ABBA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, actioned of detecting the novel polypeptides. Completely of the nucleotides of the invention. Although novel, many of the bild op polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activity; activity; tissue growth activity; immunomodulatory activity; tissue growth activities; communomodulatory activity; activity; tissue growth activities; chamchactic or chamchackinetic activities; haemostatic, thrombotic or thrombolytic activities; raceptor or lighned activities; or may be involved in oncogenesis receptor or lighned activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include canners, haematopolestic disorders (e.g., orstoporosis), and abnormal cascular growth. Polypeptides involved with tissue regeneration and cascular growth. Polypeptides involved with tissue regeneration and fugal infections in addition to immune disorders; partivities may be used in the treatment of viral, munuomodulatory activities may be used in the treatment of viral, and fungal infections in addition to immune disorders to manipulate such prowth factor activity and prowed with the search of viral, prowth factor activity and properties with growth. For example, or immuned and cull or prevention or immune or cell cillure to give rise to meuroperies in addition or repetical sections and conditions or repetical activities may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucled may also be used in the diagnosis of the above conditions, and in discreening techniques. The present sequence represents a novel human
                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1028; DB 22; Length 1435; 100.0%; Pred. No. 7.6e-65; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 256-257; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide of the invention
                                                                                                                                                                                                                                           Drmanac RT
                                                                     05-FEB-2001; 2001WO-US03800
                                                                                                                  03-FEB-2000; 2000US-0496914, 27-APR-2000; 2000US-0560875.
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               QGSNSSSADPKAPPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                      cell proliferation; cell differentiation; gene therapy; therapy; stem cell growth factor; haematopoiesis; tor; immunomodulatory; cancer; leukaemia; sorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this patent did not form part of the printed in electronic format directly from WIPO
QGSNSSSADPKAPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids and polypeptides, useful for preventing eating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO 19747; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 277; DB 22;
Pred. No. 1.7e-12;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did specification, but was obtained in electroniat ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                  Protein; 140 AA
                                                                                                                                                                                                                                                            SEQ ID NO 19747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.9%;
Best Local Similarity 91.4%;
Matches 53; Conservative
                                                       EFTGAQSGGPQONP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO-US04927
                                                                                                                                                                                                                              st entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /56.
                                                                                                                                                                 AAO05855 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA;
                                                                                                                                                                                                                             (fir
                                                                                                                                                                                                                                                                                                     vaccine; peptide
tissue growth fac
                                                                                                                                                                                                                                                                                                                                    nervous system di
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001
                                                                                                                                                                                                                                                           Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic diagnosing and tradisorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-514838,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI85786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID
                                                                                                                                                                                                                                                                                        cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                               WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001.
                                                                                                                                                                                                                             06-NOV-2001
                          359
                                                                                                                                                                                              AA005855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                     419
                                                          181
                                                                                                                                  RESULT 3
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PIPAPAPKPAAPPRPLDRESP--GVENKLIP-SVGSPASSTPLPPDGTGPNSTPNNRAVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSQGSNSSSADPKA--PPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence course beta-catenin nuclear localised protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 232.5; DB 2 35.1%; Pred. No. 5.7e-09;
                                                                                                                                                                                      beta-catenin nuclear localised protein;
                                                                                                                                        Mouse beta-catenin nuclear localised protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                                                                                                                                                                 gene therapy; EST; expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 91-92; 113pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78460 standard; Protein; 1494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F--PDEKEFT----GAQSGGP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRSGETEPFLKGPPGGAGEGGP 196
   A
AAU78461 standard; Protein; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-2000; 2000JP-0287876.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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tes 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK47632
                                                                                                                                                                                                                                                                                                      WO200224738-A1
                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-2001;
                                                                                                                                                                                                                                                              Mus musculus
                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                        28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78460
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 QSGPKP-PIPPPPPQQQQPPPQQPPPQQPPPQPPPQPPQPPQQQQPPVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 RNDPKPLPQQPPAPANQDQN--SSQNTRLQPTPPIPAPAPKP----AAPPRPLDRESPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EN--KLIPSVGS--PASSTPLP-----PDGTGPNSTPN-NRAVTPVSQGSNSSSADP
  amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating disorders
                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167.5; DB 22;
Pred. No. 0.00053;
5; Mismatches 47;
                                                                                                                                                                                                                                                                                                              Chen R, Ma Y, C
Xu C, Xue AJ,
, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 2286; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, us such as central nervous system injuries
                                                                                                                                                                                                                                                                                                             Chen R,
                                                                                                                                                                                                                                                                                                            Asundi V, Che
Wehrman T, Xi
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                           ; 2000US-0488725.
; 2000US-055317.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.3%;
ilarity 40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| | ||| | |
163 GAPPTPPSSGVPTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAPPPPPVSSGEPPT 145
                                                                                                                                    26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47
N-PSDB; AAI58297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                         Zhou P,
                                                                                                                                                                                                                                                                                                             Liu C,
Wang Z,
                                                                                WO200153312-A1
                                                                                                                                                           21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                            Tang YT,
Wang J, W
                             leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                         New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 SILAYHQQNVPRAKLDQA------PKVPPTPEPLPLN---TPSAGTPQSQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PIPAPAPKPAAPPRPLDRESP--GVENKLIP-SVGSPASSTPLPPDGTGPNSTPNNRAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 PVSQGSNSSSADPKA--PPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence c mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 232,5; DB 23; Lung-
Pred. No. 2.7e-08;
                                                     localised protein; cancer; sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Mismatches
                                                                   expressed sequence
                           nuclear localised
                                                                                                                                                                                                                                                                                                                                                                              88; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F--PDEKEFT----GAQSGGP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 707
                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.6%;
35.1%;
                                                                                                                                                                         19-SEP-2001; 2001WO-JP08140.
                                                                                                                                                                                                  22-SEP-2000; 2000JP-0287876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
  st entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                        Adachi S;
                                                                                                                                                                                                                                                                                   .36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                     in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
                         Mouse beta-cateni
                                                     beta-caten
                                                                   gene therapy; EST
                                                                                                                                                                                                                                                                                WPI; 2002-330014,
N-PSDB; ABK47631,
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 81
                                                                                                                                                                                                                                                                                                                        New beta-catenin
                                                                                                                      WO200224738-A1
                                                                                              Mus musculus.
                                                                                                                                                28-MAR-2002.
 02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                        Akiyama
                                                    Mouse;
                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM39141
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WO200144292-A2
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                                                                                                                                                                                                           (CURI-) INST
                                                                                                                                                                                                                                           Noireaux V,
Louvard D;
            13-NOV-2001
                                                                                                                                                                                       16-DEC-1999;
                                                                                                                                            21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG27250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for identifying modulators of actin polymerisation. The method involves using proteins that contain at least one binding motif for proteins of the Ena/VASP (vasodilator-stimulated phosphoprotein) family in the preparation of reagents for identification/screening of molecules that modulate formation of the actin cytoskeleton. The proteins used in the method (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not bind to the Arp2/3 protein complex. The modulators identified by the method are potentially useful for treating disorders of actin polymerisation, e.g. metastatic cancer or parasitic infection; and as cytotoxic agents. The present sequence one such protein with binding motif(s) for Ena/VASP proteins, which was used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 IAPVSMNPAINSTSKPPLPPPSSRVSAAALAANKKRPPPPPPPSRRNRGKPPIGNGSSNS
                                                                                      lon; Ena/VASP; vasodilator-stimulated phosphoprotein;
parasitic infection; cytotoxic; WASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                     Identifying modulators of actin polymerization, potentially useful treating tumor metastasis and parasitic infection, using proteins
                                                                                                                                                                                                                                                                   Noireaux V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 162.5; DB 22; Length 574; 30.9%; Pred. No. 0.00097; tive 21; Mismatches 64; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louvard D,
                                                                                                                                                                                                                                                                   Golsteyn RM,
                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Pages 107-109; 109pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 574 AA.
574 AA
                                                                                                                                                                                                                                                                                                                                            binding sites
                                                                                                                                                                                      21-MAR-2001; 2001WO-FR00843
                                                                                                                                                                                                                                                           Fradelizi J, Friederich E,
Sykes C;
                                                                                                                                                                                                           22-MAR-2000; 2000FR-0003637
                                            (first entry)
                                                                                                                                                                                                                                (CURI-) CENT NAT RECH SCI.
                                                                                                                      Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                protein.
                                                                                                                                                                                                                                                                                                  73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG67370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic agents.
motif(s) for Ena/
present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 RLQPTPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 AA
                                                                                      Actin polymerisat
metastatic cancer
AAM52322 standard
                                                                                                                                                                                                                                                                                               WPI; 2001-639148/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPGRSAP-
                                                                                                                                                                                                                                                                                                                                 treating tumor me
contain Ena/VASp
                                                                                                                                          WO200171356-A2.
                                                               WASP homolog
                                           18-JAN-2002
                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                    AAM52322
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AAG67370
ID AAG6
XX
AC AAG6
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335 SLPPPPPPPRSNAAGSIPLPPQGRSAPPPPPPRSAPSTGRQPPPLSSSRAVSNPPAPPPA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a WASP (Wiskott-Aldrich syndrome protein) homologue. Peptide fragments of WASP-family proteins of eukaryotic cells are used to prepare reagents for detecting compounds that inhibit or stimulate formation of the actin cytoskeleton, and thus inhibit or stimulate cell motility. The peptides are used to detect and identify compounds which are potentially useful for treating diseases associated with dysfunction of actin polymerisation, particularly metastatic cancer and parasite infection; as cytotoxic agents for inhibiting/stimulating formation of the actin cytoskeleton and for detecting side-effects, on actin polymerisation, of pharmaceuticals. By modulating actin polymerisation, these compounds affect cell motility, embryonic development, the immune response and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IQNISNNKTERSTA-----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fragments of WASP family proteins, useful for detecting and identifying modulators of actin cytoskeleton formation, potential anticancer and antiparasitic agents
                                                                                                                     Wiskott-Aldrich syndrome protein; WASP; actin cytoskeleton; cell motility; actin polymerisation; cancer; parasite infection; embryonic development; immune response; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Golsteyn RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                             Amino acid sequence of a yeast WASP protein homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friederich E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162.5; DB
Pred. No. 0.00097
21; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG27250 standard; Protein; 406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sykes C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Fig 8; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%;
30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2000; 2000WO-FR03569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99FR-0015900
(first entry)
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Best Local Similarity 30.99
                                                                                                                                                                                                                                                  Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prost J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-536241/59.
N-PSDB; AAH77922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 AA;
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18-AUG-1999;
28-SEP-1999;
                                                                  14-APR-2003
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                                                                                                                                                                                 22-FEB-2001
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                                                                                                                                                                                                                                                                                      Wiemann
                                                                                                                                       Ношо
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ABU52939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                              lates to isolated polynucleotide (I) and sequences. (I) is useful as hybridisation probes, reaction (PCR) primers, oligomers, and for chromosome, and in recombinant production of (II). The are also used in diagnostics as expressed sequence tags expressed genes. (I) is useful in gene therapy techniques I activity of (II) or to treat disease states involving eful for generating antibodies against it, detecting or olypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NODONSSONTRLOPTPPIPAPAPKPA-APPRPLDRESPGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPASSTPLPPDGTGPNSTP-NNRAVTPVSQGSNSSSADPKAPPPPVSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity .
                                              forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                             therapy; forensic
genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        data for this patent did not appear in the was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159, DB 22;
Pred. No. 0.0012;
15; Mismatches 62;
                                             j; gene mapping; gene
imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                          No 57609; 103pp; English
                    Novel human diagnostic protein #27241
                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.5%;
32.0%;
                                                                                                                                                                    US-0540217.
                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                             mapping;
nedical in
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 PKPLPQQPPAPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data
                                                                                                                                                                                                                                                                                                                                                                   relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                  73.
                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                             The invention related polypeptide (II) sepolymerase chain reand gene mapping, a polynucleotides are for identifying exptorestore normal a (II). (II) is useful quantitating a poly a food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                    31-MAR-2000; 20000
23-AUG-2000; 20000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence
specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 N-KLIPSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: :||
PPSPSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPSPPPSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 AA
                                             chromosome
                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 PPTLGENP
                                                                                                                                                                                                                                                 WPI; 2001-639362/
N-PSDB; AAS91437.
                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID
                                           Human; chromosom/food supplement;
                                                                                                 WO200175067-A2
                                                                            Homo sapiens
                                                                                                                                                                                                                            RT,
18-FEB-2002
                                                                                                                        11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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a
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from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity, The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 KSSPPPAPVNLPPPEVKSSPPPTPVSSPPPAPKSSPPPAPMSSPPPFVKSPPPPAPVSS 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP---TPPIPAPAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-----PDGTGPNSTPNNRAVTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                           Human mammary carcinoma-derived DKFZphmcf1_1c23 homologue #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mammary carcinoma-derived DKF2phmcf1_1c23 homologue #9.
                                                                                                                                                                                                                                     Human; gene therapy; vaccine; disease treatment; detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 158.5; DB 22;
; Pred. No. 0.00082;
17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example III; Page 551; 1095pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHU-) GERMAN HUMAN GENOME PROJECT.
ABU52945 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU52939 standard; Protein; 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-IB01496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0149499
99US-0156503
                                                                                                                  (first entry)
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AA;
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N-PSDB; ABL14166
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                                                              (PEKE ) PE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytoskeleton;
                            23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                         11-JUL-2000;
                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9801755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998
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                                                                                  JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW37151;
                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                  Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                            This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSSPPPAPVNLPPPEVKSSPPPTPVSSPPPAPKSSPPPAPMSSPPPPEVKSPPPAPVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPPVKSPPPAAPVSSPPPPVKS---PPPPAAPVSSPPPPAKSPPPAAPISSPPPVKSPP 195
                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                           14 KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP---TPPIPAPAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- PDGTGPNSTPNNRAVTPV
                                                                                                                                                                                                         Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                15.4%; Score 158.5; DB 22; Length 270; 32.0%; Pred. No. 0.00087; Live 17; Mismatches 68; Indels 19;
         Human; gene therapy; vaccine; disease treatment; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 36981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPAPVSSPPPPVKSPPPAPVSSPPPIKSPPP
                                                                                                                                                                                                                                          English
                                                                                                                                             (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 446
                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                         550; 1095pp;
                                                                                          L8-AUG-2000; 2000WO-IB01496
                                                                                                               99US-0149499
99US-0156503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                      WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB70063 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                             270 AA
                                                                                                                                                                                                                                         Example III; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                  WO200112659-A2
                             Homo sapiens,
                                                                                                              18-AUG-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                      22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sim
Matches 49;
                                                                                                                                                                  Wiemann S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
ABB70063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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145 YGPPQTPPPRPPQPTPSAPAPPSYGPPQTPPRPPPQPTPSAPAPSYGPPQPPAPQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                1000 or more
and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPA--PKPAAPPRPLDRESPGVENKLIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mena+ protein; mammalian Ena; Enabled protein; Ev1 protein; eleton; cell morphology; cell adhesion; cell differentiation; rowth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 36981; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                          detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 158.5; DB 22;
Pred. No. 0.0014;
1; Mismatches 64;
                                                                                                                                                                                   E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "encoded by GGN"
                                                                                                                                                                                   Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGEPPTLGENPDGLSQEQLEHR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||: |: |: | : | PPSPPSPQPGPEYLPPDQPKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.48; 29.68;
                                                  2000US-191637P
2000US-0614150
23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mena+ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 29.6
42; Conservative
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                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                 2001-656860/75
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                                                                                                                                                                                                                                                                                                           This protein comprises novel murine neural Mena+. Its amino acid sequence was deduced from a CDNA clone (see AAV02998) obtained from a mouse brain cDNA library. Neural Mena+ contains an exon that introduces 244 amino acids between amino acids 238 and 239 of mammalian Ena (Mena, see AAW37148). Two other isoforms, neural Mena++ (see AAW37152) and neural Mena+++ (see AAW37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Evl genes (see also AAV02996-97) and proteins (see also AAW37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 NKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSHCGSQASPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                    Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neural Mena++ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPAESPTPQG -- LVLGPPAPPPPPPPPPSGPAYASALPPPPGPPP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TPVSQGSNSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 158; DB 19;
Pred. No. 0.0028;
5; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QISALRNDP--
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                                                                                                                             Wehland
                                                                            FORSCHUNG MBH
CENT FRED.
                                                                                                                                                                                                                                                                                 58-60; 77pp; English
                                                                                                                             Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                           GES BIOTECHNOLOGISCHE HUTCHINSON CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.4%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mena++ protein.
              97WO-US11669
                                            96US-0675815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DRESPGVENKLI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 KPLPQQPPAPANQDQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.3
Matches 59; Conservative
                                                                                                                         Gertler FB, Niebuhr K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 NKTERSTAPLNT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783 AA
                                                                                                                                                     WPI; 1998-101197,
N-PSDB; AAV02998
                                                                                                                                                                                                                                                                                    Example 4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse neural
              03-JUL-1997;
                                            05-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                          (GBFB)
                                                                                         (HUTC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claimed
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AAW37152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW371
QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
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452
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                                                                                                                                                                                                                                                                                                                                                                      This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a cDNA clone obtained from a mouse brain cDNA library. Two other isoforms, neural Mena+ (see AAW37151) and neural Mena+++ (see AAW37153), are also disclosed. Unlike mammalian Ena (Mena, see AAW37148), neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Evl genes (see also AAV02996-98) and proteins (see also AAW37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 NKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPLPQQPPAPANQDQN-----SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 158; DB 19;
26.3%; Pred. No. 0.0028;
ive 15; Mismatches 62;
                                                                                                                                                                                                                <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --QISALRNDP-
                                                                                                                                                                                                                Wehland
                                                                                                                                                                   FORSCHUNG MBH
CENT FRED.
                                                                                                                                                                                                                                                                                                                                           Example 4; Page 60-63; 77pp; English.
                                                                                                                                                                                                               Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 802
                                                                                                                                                                (GBFB ) GES BIOTECHNOLOGISCHE (HUTC-) HUTCHINSON CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse neural Mena+++ protein.
                                                                                                                                    96US-0675815
                                                                                                        97WO-US11669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.39
Matches 59; Conservative
                                                                                                                                                                                                               Gertler FB, Niebuhr K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKTERSTAPLNT
                                                                                                                                                                                                                                         WPI; 1998-101197/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         787 AA;
                                                                                                                                                                                                                                                                                                                   differentiation
               Mus musculus
                                          WO9801755-A1
                                                                                                    03-JUL-1997;
                                                                                                                                   05-JUL-1996;
                                                                         15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                  Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
Otein; mammalian Ena; Enabled protein; Ev1 protein; morphology; cell adhesion; cell differentiation; motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 158; DB 19; Length 802; llarity 26.3%; Pred. No. 0.0028; Conservative 15; Mismatches 62; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 QPAESPTPQG--LVLGPPAPPPPPLPSGPAYASALPPPPGPPP 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QISALRNDP--
                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                            Wehland
                                                                                                                                                                                                             (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 63-65; 77pp; English.
                                                                                                                                                                                                                                                            Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPLPQQPPAPANQDQN---
                                                                                                                                                    97WO-US11669.
                                                                                                                                                                                96us-0675815
                                                                                                                                                                                                                                                         Gertler FB, Niebuhr K,
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                                                                                                                                                                                                                                                                                       .09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 59; Conserv
  cytoskeleton; cell
cell growth; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                       WPI; 1998-101197,
                                                                                                                                                                                                                                                                                                                                                                  differentiation
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                                                                                                                                                                                                                                                                                                                      Detection of
                                                                                                                                                    03-JUL-1997;
                                                                                                                                                                                  05-JUL-1996;
                                                             Mus musculus
                                                                                         W09801755-A1
                                                                                                                     15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348
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Search completed: October 15, 2003, 10:30:25 Job time: 120.268 secs

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October 15, 2003, 10:27:32; Search time 39.2529 Seconds (without alignments) 209.113 Million cell updates/sec
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Compugen Ltd
  version
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1 TIVSFHIQNISNNKTERSTA.
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             Copyright
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Sequence:
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seqs, 42310858 residues 462 10.0 , Gapext 0.5 BLOSUM(Gapop 328717 Scoring table:

satisfying chosen parameters: hits of Total number

um Match 0% um Match 100% ng first 45 summaries 2000000000 Minimum Maximum Maximum Misting 1 length: length: Post-processing: sed DB DB Minimum Maximum

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the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution. e greater tis derived ţs Š. Pred. score and is

Sequence 12, Appli Sequence 2, Appli Sequence 7, Appli Sequence 4, Appli Sequence 32, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 24873, A Sequence 2, Appli Sequence 2, Appli Sequence 53, Appli 84, Appl 74, Appl 58, Appl 104, App Sequence 44, Appl Sequence 42, Appl Sequence 84 Sequence 74 Sequence 14 Description Sequence Sequence Sequence Sequence US-07-952-800-2 US-08-764-870-7 US-08-980-115-7 US-07-952-800-4 US-08-980-115-7 US-08-580-5458-6 US-08-580-5458-6 US-09-262-653A-6 US-09-252-9013-1 US-09-252-91A-24873 US-09-080-897-2 US-09-080-897-2 US-09-080-897-2 US-09-080-897-2 US-09-080-897-2 US-09-056-556-53 US-09-056-556-53 US-09-056-556-53 US-07-757-0228-14 US-07-757-0228-104 SUMMARIES Length DB 84555333 84555333 84555333 84556 84556 84566 84566 84566 84566 846 % Query Match 1001.5 10

, Appl

Sequence 60, Appl Sequence 48, Appl Sequence 40, Appl Sequence 52, Appl Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 14, Appli Sequence 10, Appli Sequence 2, Appli	Sequence 3
US-07-757-022B-60 US-07-757-022B-48 US-07-757-022B-40 US-07-757-022B-52 US-07-757-022B-2 US-08-999-595-3 US-08-999-595-3 US-08-899-595-3 US-08-177-327-4 5202236-37 US-08-17-327-4 5202236-37 US-08-11-41 US-09-514-247A-10 US-08-132-528-2 US-09-132-528-3 US-09-132-528-3 US-09-132-528-3 US-09-132-528-3	US-09-599-366-3
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133.55 133.55 133.55 133.55 132.55 130.55 130.55 130.55	130.5
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ALIGNMENTS

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Sequence 12, Application US/09266225D

Sequence 12, Application US/09266225D

Patent No. 6573364

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishan

APPLICANT: Kingsmore, Stephen

APPLICANT: Tchernev, Velizar

ITTLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak

TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein:

ITTLE OF INVENTION: Interacting Proteins

FILE REFERENCE: 15966-523

CURRENT APPLICATION NUMBER: US/09/266,225D

CURRENT FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 RSTAPLNTQISALRNDPKPLP------QQPPAPANQDQNSSQNTRLQPTPPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637 GPAPHPTGPPGPIPVPAPPQIATSTSLLAAQSLVPPPGLPGSSTPGVLPYFPPGLPPDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 RPAAPALTSVPAPAPAPTPTPTPTVQPTSPPPGPVAQPTGPQPSAGSTSGPVPQPACPPP
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Patent No. 5403925
GENERAL INFORMATION:
APPLICANT: OZATO, KEIKO
TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE
TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CLONE THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAPQSSMSESPDVNLVT--QQLSKSQVEDPL----PPVFSGTPKGSG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 G--PNS----TPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 APAPKPAAPPRPLDRESPG-----VENKLIPSVGSPASSTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 161.5; DB 4;
Pred. No. 1.6e-05;
7; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-266-225D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1
US-09-266-225D-12
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 12
LENGTH: 816
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US-07-952-800-2
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RESULT 4
US-08-980-115-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PKPAAPPRPLDRESP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 533;
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Binding Domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3000 El Camino Real
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000 CITY: SAN FRANCISCO STATE: CA
                                                                  ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,800
FILING DATE: 19920928
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JABLE FORM:
3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.6%; Score 150.5; DB 1
Best Local Similarity 31.0%; Pred. No. 7.7e-05;
Matches 40; Conservative 11; Mismatches 45
                                                                                                                                                                                                                                                                                                                               15280-21-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08764870
Sequence 7, Application US/08764870
Fatent No. 6236946
GENERAL INFORMATION:
APPLICANT: Baxter, John D
APPLICANT: Fletterick, Robert J
APPLICANT: Fletterick, Robert J
APPLICANT: Wagner, Richard L
APPLICANT: Wagner, Peter J
APPLICANT: West, Brian
ITTLE OF INVENTION: Binding Domain
ITTLE OF INVENTION: Binding Domain
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square,
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ley Godward
alo Alto Square,
                                                                                                                                                                                                                                                          ATORNEY AGENT INFORMATION:

NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 1528(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | | CPPPPGGPG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE MEDIUM TYPE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE:
US-07-952-800-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94306
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                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-764-870-7
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Sequence 7, Application US/08980115

Sequence 7, Application US/08980115

Patent No. 626662

GENERAL INFORMATION:

APPLICANT: Scanlar, Thomas S.

APPLICANT: Baxter, John D.

APPLICANT: Hetterick, Robert J.

APPLICANT: Magner, Richard L.

APPLICANT: Magner, Brian L.

APPLICANT: Magner, US/08/980,115

CURRENT APPLICATION NUMBER: US/08/4,870

EARLIER APPLICATION NUMBER: 60/008,606

EARLIER APPLICATION NUMBER: 60/008,540

EARLIER APPLICATION NUMBER: 60/008,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | |||| ||:|
78 SSPNPLPQGVPPPSPPG------PPLPPSTAPTLGGSGAPPPPMPPPPLGSPFP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PKPAAPPRPLDRESP
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Pred. No. 9.1e-05;
0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-
                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
APPLICATION NUMBER: USAL-246/01US
TELECOMMUNICATION INFORMATION:
13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 31.0%; Pr
Matches 40; Conservative 10;
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 13-DEC-19
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-764-870-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 -PPPPVSSG 141
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Matches
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                                                                                                                                                                                                                                               127 VISS----SMGSPGLPPPAPPGFSGPVSSPQINSTVSLPGGGSGPPEDVKPPVLGVRGLH 182
                                                                                                                                                                                                                          31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPRPLDRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- QPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR HORMONE
AND A CDNA CLONE THEREOF
                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                             82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP-
                                                                                                                                                           Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 446;
                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OZATO, KEIKO
TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMON
TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CL.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,800
FILING DATE: 19920928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 143.5; DB 1; 30.3%; Pred. No. 0.00023; tive 12; Mismatches 44;
                                                                                                                                                      Query Match 14.5%; Score 149.5; DB 3; Best Local Similarity 31.0%; Pred. No. 9.1e-05; Matches 40; Conservative 10; Mismatches 46;
                                                                                                    minimal ligand binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15280-21-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on US/07952800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO: 4: RISTICS:
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                                                                                                                                                                                                                                                                                                                                                                 134 -PPPPVSSG 141
                                                                                                                                                                                                                                                                                                                                                                                                 183 CPPPPGGPG 191
                 TYPE: PRT
ORGANISM: Homo sapiens
                                                               NAME/KEY: DOMAIN

COCATION: (292)..(523)

COTHER INFORMATION: min

US-08-980-115-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-07-952-800-4
; Sequence 4, Applicatio
; Patent No. 5403925
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-5-E
TELEFAX: 415-543
INFORMATION FOR SEQ 1
SEQUENCE CHARACTER1
LENGTH: 446 amin
TYPE: AMINO ACIC
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION
APPLICATION NUMBI
FILING DATE: 199
CLASSIFICATION:
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Best Local Similarity
Matches 37; Conser
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COMPUTER READABLE
MEDIUM TYPE: F1
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; MOLECULE TYPE:
US-07-952-800-4
LENGTH: 525
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APPLICANT: Swidth Janet
APPLICANT: Yother, Janet
APPLICANT: Tother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Tart, Rebecca
TITLE OF INVENTION: PNETMOCOCCAL GENES, PORTIONS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                        64 APAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
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 PSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSSSADPKAPPPPVSSGEPPTLGENPD----GLSQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 140.5; DB 4;
Pred. No. 0.014;
); Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                  Sequence 32, Application US/08714741 Patent No. 6500613
                                                                                                                                                                                                                                                                          Briles, David E. McDaniel, Larry S. Swiatlo, Edwin Yother, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 13.7%;
1 Similarity 27.4%;
43; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
                                                                           140 SG 141
                                                                                                                    PG 112
                                                                                                                                                                             RESULT 6
US-08-714-741-32
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89
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                         APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
   APAPKPEKPAEKPAPAPKPETPKTGWKQE 6090
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,545B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 0.00038;
9; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04473/068001
                                                                                                                                                                                                      TITLE OF INVENTION: COTTON FIBER TIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 601 Thirteenth Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/783-5070
TELEFAX: 202/783-2331
                                                                              on US/08580545B
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Koichi, Fujisawa
Susumu, Nishiguchi
Yoshihiko, Maekawa
Randy, Allen
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ilarity 31.2%;
Conservative
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Patent No. 6166294
GENERAL INFORMATION:
APPLICANT: Yoshihis
APPLICANT: Susumu,
APPLICANT: Yoshihis
APPLICANT: Randy, 1
                                                                            Sequence 6, Applicatic
Patent No. 5932713
GENERAL INFORMATION:
APPLICANT: YOSHIHI
                                                                                                                                                                                                                                                            ADDA...
STREET: burrary: Washingtor
                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005
COMPUTER READABLE 1
MEDIUM TYPE: Flo
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amino aci
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Best Local Similarity
Matches 43; Conser
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INFORMATION FOR SEQ
SEQUENCE CHARACTER
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   --APAPAP
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CLASSIFICATION:
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TOPOLOGY: LLI
                                                             US-08-580-545B-6
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US-09-262-653A-6
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US-08-580-545B-6
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9509
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73 PRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPI--PAPAPKPAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                               COTTON FIBER TISSUE-SPECIFIC GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,012
FILLING DATE: 17-MAD-10.2
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 138.5; DB 3;
Pred. No. 0.00038;
9; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                   04473/068001
                                                                                                                                                                                                                                                NUMBER OF INVENTION: COTTON FIBER TISS NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 601 Thirteenth Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08819013
; Patent No. 5994522
; GENERAL INFORMATION:
    APPLICANT: Chan, Andrew C.
    TITLE OF INVENTION: BLNK PROTEINS
; NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Flehr, Hohbach, Test, Al
    STREET: Four Embarcadero Center, Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 PPPPVSSGEPPTLGENP 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: 11-
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CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.2
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-262-653A-6
                                                                                                                                                          20005
                                                                                                                                             COUNTRY:
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- 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634 PPLPEGVGIPSPSSLPGGTAIPP----PPPLPGSARIPPPPPLPGSAGIPPPPPLPGE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 PLPQQ-----PPAPANQDQNSSQNTRLQPTPPIPAPAPKPA----APPRPLDRES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
   63 PPVPPSPEPSPEP-PVPPSSPPV----PGVPPSPPPVPP--SPPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1248;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Date: DC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
FILING DATE:
CLASSIFICATION:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENSORM: 1748 amiting acide
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Pred. No. 0.0029;
8; Mismatches 59;
                                                           120 SQGSNSSSADPKAPPPPVSSGEPPTLGENPDG 152
                                                                                        --PPVPPSPPPS--PPPPVPPSPPG 127
                                                                                                                                                                                                                                                                                                                                                                                                STREET: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     Sequence 2, Application US/09080897 Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09323735 Patent No. 6197932
                                                                                                                                                                                                                                                             King, Mary-Claire
Lynch, Eric D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.3%;
Best Local Similarity 32.3%;
Matches 43; Conservative
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APPLICANT: King,
APPLICANT: Lynch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-09-080-897-2
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US-09-323-735-2
                                                                                                                                                              RESULT 11
US-09-080-897-2
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Sequence 24873, Application US/09252991A
Sequent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24873
LENGTH: 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 IDNRSSQRHSPPPS-----KTLPSKPSWP-----SEKARLTSTLPALTALQKP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGSNSSSADPKAPPP----PPVSSGEPPTL-----GENPDGLSQEQ-- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 OVPPKPKGLLEDEADYVVPVEDNDENYIHPTESSSPPPEKAPMVNRSTKPNSS----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAPPRP --- LDRESPGV ---- ENKLIPSVGS -- PASSIPLPPDGTGPNSTPNNRAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IQNISNNKTERSTAPL-----NTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 136.5; DB 4; 26.8%; Pred. No. 0.00023; ive 19; Mismatches 36;
 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/788,322
FILING DATE: 24-JAN-1997
ATORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-64383-1/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 VQAFCSDSSKPGTLSLPNGLFFTNAQLSSLQPPCKPVP
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 137; DB 2;
; Pred. No. 0.00083;
26; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 PAERHRGSSHRQEAVQS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LEHRERSLQT 167
                                                                                                                                                                                                                                                                                                                                                                                                                     13.3%;
25.9%;
                                                                                                                                                                                                                                        ID NO: 1:
RISTICS:
                                                                                                                                                                                                                                                                               ino acids
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.3'
Best Local Similarity 25.9'
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                      unknown
435
DATA:
                                                                                                                                                                                          TELEFAX: (415) 3 TELEX: 910 27729 INFORMATION FOR SEQ I SEQUENCE CHARACTERI LENGTH: 456 amin TYPE: amino acid STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 41; Conser
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US-09-252-991A-24873
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MOLECULE TYPE:
US-08-819-013-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 136.5; DB 3; Length 1248; 32.3%; Pred. No. 0.0029; tive 8; Mismatches 59; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eved, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                       DABLE FORM:

E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
          APPLICANT: Lynch, Eric D.
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Welcsh, Piri L.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UW97-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-818-112-53
; Sequence 53, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORIEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 Mary-Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGEPPTLGENPDG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                        COMPUTER READABLE FOR MEDIUM TYPE: Flopp COMPUTER: IBM PC COPERATING SYSTEM: SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o acid
linear
King, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEC
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US-09-323-735-2
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TOPOLOGY:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
TITLE OF I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 HIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 HMHQVDPNLTRRKGRLAALAIAAMAS-ASLVTVAVPATANADP------EPAPPVPTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Indels
                                                                                                                                                          COUNTRIE USA

ZUDIA 198104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 135; DB 3; 27.6%; Pred. No. 0.00084; tive 15; Mismatches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AASPPSTAAAPPAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98104-7092
                                                                                                 CITY: Seattle
STATE: Washingt
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 63
CITY: Seat
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US-08-818-112-53
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US-08-818-111-53
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Gaps

38;

Length 332; Indels 57

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66 APKP----AAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQ 121
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                                                                                                                                                                             Query Match 13.1%; Score 135; DB 4; Best Local Similarity 27.6%; Pred. No. 0.00084; Matches 42; Conservative 15; Mismatches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
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Job time : 40.2529 secs
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMHQVDPNLTRRKGRLAALAIAAMAS-ASLVTVAVPATANADP-----EPAPPVPTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Washington
COUNTRY: USA
ZIP: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.1%; Score 135; DB 4; Length 332; Best Local Similarity 27.6%; Pred. No. 0.00084; Matches 42; Conservative 15; Mismatches 57; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J:
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT to avid J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
"FTEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBER: US/09/056,556
07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AASPPSTAAAPPAP-----
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acta
STRANDEDNESS: single
mobology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 APKP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-056-556-53
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US-08-818-111-53
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OM protein - protein search, using sw model

October 15, 2003, 10:32:06; Search time 82.2802 Seconds (without alignments) 379.908 Million cell updates/sec Run on:

US-09-915-543-15_COPY_199_392 1028 1 TIVSFHIQNISNNKTERSTA......LFPDEKEFTGAQSGGPQQNP 194 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

seqs, 161128416 residues

600653

Searched:

20000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA

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10: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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16: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Sequence 15. Appl	Sequence 5, Appli	Segmence 278, App	Sequence 76. Appl	Seguence 38. Appl	Sequence 2. Appli	Sequence 17. Appl	Segmence 86 Anni	Sequence 2, Appli	Seguence 2. Appli	Seguence 2. Appli	Segmence 1068. Ap	Sequence 1068. An	Segmence 1068. An	Sequence 24, Appl
DO LA CHIERO D			ID	US-10-322-579-15	US-10-322-579-5	US-09-919-039-278	US-10-168-097A-76	US-10-239-431A-38	US-09-823-240-2	US-10-086-464-17	US-10-021-660-86	US-10-078-547-2	US-09-922-226-2	US-10-098-184-2	US-09-922-217-1068	US-09-833-263-1068	US-10-025-380-1068	US-10-078-547-24
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			Match Length DB 1	1426	35	707	574	574	802	731	509	503	533	533	5179	5179	5179	507
	æ	Query	Match	100.0	17.3	16.3	15.8	15.8	15.4	15.0	14.8	14.7	14.6	14.6	14.6	14.6	14.6	14.5
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Sequence 8, Appli Sequence 22, Appl Sequence 10, Appl Sequence 766, Ap	Sequence 5, Appil Sequence 282, App Sequence 12, Appil Sequence 32, Appil Sequence 70, Appil	0000404	2, 4 4, 4 11982 37,	Sequence 53, Appl Sequence 41, Appl Sequence 700, App Sequence 1633, Ap Sequence 20, Appl Sequence 18, Appl Sequence 18, Appl
14 US-10-086-464-8 12 US-10-239-431A-22 12 US-10-239-431A-10 14 US-10-156-761-7663		16 US-10-080-170-640 12 US-10-168-097A-56 12 US-10-239-431A-36 12 US-10-168-097A-46 12 US-10-239-431A-35 15 US-10-038-010-4		12 US-10-193-002-53 12 US-10-098-732A-41 9 US-09-925-297-700 10 US-09-925-300-1633 12 US-10-240-154-20 12 US-10-240-154-18 11 US-09-917-384-1
		666 505 501 501 638 1		332 332 200 668 1668 1228
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ALIGNMENTS

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Sequence 15, Application US/1032579

Publication No. US20030114413A1

GENERAL INFORMATION:

APPLICANT: BASIER, Konrad

APPLICANT: BRUNNER, Erich

APPLICANT: BRUNNER, Erich

APPLICANT: FROESCH, Barbara

APPLICANT: FROESCH, Barbara

APPLICANT: FROESCH, Barbara

APPLICANT: FROESCH, BARDARA

TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

CURRENT APPLICATION NUMBER: US/10/322,579

CURRENT APPLICATION NUMBER: US/09/915,543

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 155

LENGTH: 1426

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  loo.0%; Score 1028; DB 15; Length 1426; Similarity 100.0%; Pred. No. 7.9e-59; Conservative 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human lgs/bcl9
US-10-322-579-15
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Sequence 38, Application US/10239431A

Sequence 38, Application US/20030170726A1

publication No. US20030170726A1

GENERAL INFORMATION:

APPLICANT: FRIEDERIZE, JULIE

APPLICANT: GOLSTEYN, ROY M.

APPLICANT: LOUVARD, DANIEL

APPLICANT: LOUVARD, DANIEL

APPLICANT: NOIREAUX, VINCENT

APPLICANT: NOIREAUX, VINCENT

APPLICANT: NOIREAUX, VINCENT

APPLICANT: NOIREAUX, VINCENT

TITLE OF INVENTION: PETTIDE SEQUENCES COMPRISING ONE OR MORE UNITS BINDING

TITLE OF INVENTION: POROTEINS OF THE Ena/VASP FAMILY, AND THEIR USES

TITLE OF INVENTION: UNMBER: US/10/239, 431A

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PALENTIN VEF. 2.1

SOFTWARE: PALENTIN VEF. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 IAPVSMNPAINSTSKPPLPPPSSRVSAALAANKKRPPPPPPPFRRNRGKPPIGNGSSNS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 QSGPKP-PIPPPPHQQQQPPPQQPPPHQPPPHQPPHQQQQQPPPPQDSSKPVV 111
                                                                                                                      84 EN--KLIPSVGS--PASSTPLP-----PDGTGPNSTPN-NRAVTPVSQGSNSSSADP 130
                                                                                                                                                                112 AQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT-----SAPP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT 54
30 RNDPKPLPQQPPAPANQDQN--SSQNTRLQPTPPIPAPAPKP----AAPPRPLDRESPGV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 15.8%; Score 162.5; DB 12; Length 574; l Similarity 30.9%; Pred. No. 0.0041; 50; Conservative 21; Mismatches 64; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/10168097A
Publication No. US20030166245A1
GENERAL INFORMATION:
APPLICANT: CENTRE NATIONAL OF THE RECHERCHE SCIENTIFIQUE
TITLE OF INVENTION: WASP FAMILY PROTEIN FRAGMENTS, AND USES THEREOF
FILE REFERENCE: IFB99WASP
CURRENT APPLICATION NUMBER: US/10/168,097A
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 76
LENGTH: 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
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CORGANISM: Schizosaccharomyces pombe
US-10-168-097A-76
                                                                                                                                                                                                                                                 131 KAPPPPVSSGEPPT 145
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163 GAPPTPPSSGVPTT 177
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Best Local Similarity
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US-09-919-039-278

Sequence 278, Application US/09919039

Publication No. US20030108871A1

GENERAL INFORMATION:

APPLICANT: Kaser, Matthew R.

ITILE OF INVENTION:

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SOFTWARE: PERL Program

SOFTWARE: PRI

ORGANISM: Homo sapiens

HAPPLICANIE: CONTINE: CONTI
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                                QGSNSSSADPKAPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 180
                                                                 319 QGSNSSSADPKAPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.3%; Score 178; DB 15;
.larity 100.0%; Pred. No. 2.4e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-322-579-5
Sequence 5, Application US/10322579
Publication No. US20030114413A1
GENERAL INFORMATION:
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, BARDARA
TITLE OF INVENTION: THERAPEUTIC AND DIAGNO
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER: US/10/322,579
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40.0%;
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US-10-322-579-5
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; OTHER INFORMATION: Incy
US-09-919-039-278
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Best Local Similarity
Matches 35; Conserv
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Best Local S
Matches 54
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71 APPRPLDRESPGVENKLIPSVG--
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; ORGANISM: Arabidopsis thaliana
US-10-086-464-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 14.8%;
| Similarity 27.0%;
| 60; Conservative 1
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US-10-021-660-86
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                                                                                                                                                                                                                                                                                                                 47;
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LENGTH: 509
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Best Local S
Matches 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                                       55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                    335 SLPPPPPPPRSNAAGSIPLPPQGRSAPPPPPPPRSAPSTGRQPPLSSSRAVSNPPAPPA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV-
                                                                                                          7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSQNTRLQPTPPIPAPAPKPAAPPRPL-
                                                                             27;
                                                  Length 574;
                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09823240

Patent No. US20020048813A1

GENERAL INFORMATION:

APPLICANT: Frank B. Gertler

APPLICANT: James E.Bear

APPLICANT: James E.Bear

APPLICANT: James E.Bear

APPLICANT: Joseph Loureio

TITLE OF INVENTION: Methods and Products for Regulating Cell

TITLE OF INVENTION: Motility

FILE REFERENCE: M0656/7064 (HCL)

CURRENT APPLICATION NUMBER: US/09/823,240

CURRENT FILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daphne R. et al.
PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 158; DB 9; Length 802; 26.3%; Pred. No. 0.011;
tive 15; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                Indels
                                                                                                                                                                                                                                 105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                      -QISALRNDP-
                                              Score 162.5; DB Pred. No. 0.0041; 21; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
  Schizosaccharomyces pombe
                                           15.8%;
imilarity 30.9%;
; Conservative 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPLPQQPPAPANQDQN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 NKTERSTAPLNT ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-10-086-464-17
Sequence 17, Applicati;
Publication No. US2002
GENERAL INFORMATION:
APPLICANT: GORING, Da
TITLE OF INVENTION: P
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus
US-09-823-240-2
; ORGANISM: Sch
US-10-239-431A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 802
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US-09-823-240-2
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Sequence 86, Application US/10021660

| Sequence 86, Application US/10021660
| Publication No. US20030152926A1
| GENERAL INFORMATION:
| APPLICANT: Murray, Richard
| APPLICANT: Glynne, Richard
| TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
| TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
| TITLE OF INVENTION: Modulators
| TI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPK--PAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QQPPAPANQDQNS----SQNTRLQPTPPIPAPAPKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SNSSSADPKAPP-----PPPVSSGEPPTLGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 PSESTPPVNTASPPPPSPPRRRSGPKPSFPPPINS-SPPNPSPNTPSLPE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.0%; Score 154.5; DB 14; Length 731; Similarity 27.6%; Pred. No. 0.017; Conservative 20; Mismatches 68; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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Pred. No. 0.017;
3; Mismatches 65;
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRPLDRESPGVENKLIPSVGSPASSTPL----
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PPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAV--- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TPVSQGSNSSSADPK-----APPPPPPVSSGEPPTLGENPDGLSQEQLEHR-- 161
APPPPPPRSRAGSGAGALPCAGHTRRRRTSSPRSSPPLSGPPGRASPRGARPPPLLRAA 212
                                                           -----TL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SONTRL-OPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 NNKPPVPSTPRPSAPHRPH---LRPPPPSRPGPPPLPPSSSGNDETPRLPQRNLSLSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 151.5; DB 14; Length 503; 26.5%; Pred, No. 0.019; Live 25; Mismatches 84; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 FHPISDLPPPEPYVQTTKSYPSKLARNESR-SGSNRRERGGPPLPP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ERSLQTLRDIQRMLFPDEKEFTGA---QSGGPQQNP 194
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aratna, Roshantha A.
H: Methods of Screening For Compounds That
H: Modulate Hormone Receptor Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNS---
                                                                                                             147 GENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSG 188
                                                                                                                                         -TPNNRAVTPVSQGSNSSSADPKAPPPPVSSGE----PP----
                                                                                                                                                                                                                                         Sequence 2. Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
APPLICANT: Narayanaswamy Ramesh
APPLICANT: Naiguel A. de la Fuente
APPLICANT: Raif S. Geha
TITLE OF INVENTION: WIP, A WASP-Associated Profile OF INVENTION: WUBER: US/10/078,547
CURRENT APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR FILING DATE: 1998-12-22
; PRIOR FILING DATE: 1998-12-22
; PRIOR FILING DATE: 1998-09-23
; PRIOR FILING DATE: 1998-09-23
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1997-12-23
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0030077664A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application Publication No. US2003; GENERAL INFORMATION:
APPLICANT: Zhao, Yi
APPLICANT: Thacher,
APPLICANT: Xiao, Jiz
APPLICANT: Chandrare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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SOFTWARE: FASTSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQ ID NO 2
LENGTH: 503
TYPE: PRT
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US-09-922-226-2
                                                                                                                                                                                                          RESULT 9
US-10-078-547-2
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Best Local (
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Matches
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; OTHER INFORMATION: Description of Artificial Sequence; No. US20030105333Ale -; OTHER INFORMATION: Synthetic construct US-10-098-184-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP----- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                     31 NDPKPLPQ--QPPARANQDQNSSQNTRLQPTPPLPAPA-----PKPAAPPRPLDRESP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPRPLDRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                       45; Indels 33;
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                                                                                                                                                                                                                                                                                                                           Length 533;
                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10098184

publication No. US20030105333A1

GENERAL INFORMATION:

APPLICANT: Pfahl, Magnus

APPLICANT: Fachdjian, Catherine

APPLICANT: Fanjul, Andrea

APPLICANT: Fenjul, Andrea

APPLICANT: Fine, Lyle W.

APPLICANT: Fine, Richard

APPLICANT: Fine, Richard

APPLICANT: Fine, Richard

APPLICANT: Fine, Richard

APPLICANT: Spruce, Lyle W.

APPLICANT: Fine, Richard

APPLICANT: Sapf, James W.

TITLE OF INVENTION: RXR ACTIVATING MOLECULES

FILE REFERENCE: 13099.0016U2

CURRENT APPLICATION NUMBER: 60/274,342

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 533

TUBLICH: FILE
                                                                                                                                                                                                                                                                                                                       Query Match 14.6%; Score 150.5; DB Best Local Similarity 31.0%; Pred. No. 0.023; Matches 40; Conservative 11; Mismatches
FILE REFERENCE: P-AR 4681
CURRENT APPLICATION NUMBER: US/09/922,226
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/284,797
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 -PPPPVSSG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 -PPPPVSSG 141
                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Homo sapiens US-09-922-226-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-098-184-2
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; ORGANISM: Homo sapiens
US-10-025-380-1068
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Sinth, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: OF COLON CANCER AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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25.6%; Pred. No. 0.24;
Live 20; Mismatches 65;
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; Sequence 1068, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, John A.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHER
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANC
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                              Sequence 1068, Application US/09922217 Patent No. US20020076414A1
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Best Local Similarity 25.69
Matches 41; Conservative
191 CPPPGGPG 199
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US-09-922-217-1068
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                                                                                                                        1428 TTTTPPPTTTPSPPTTTTTTTTTPLPTTTPSPPTSTTTTPPPPTTTTPSPPTTTTPSP
                                                                                         TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAP--
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APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Ship, Carole L.
APPLICANT: Ship, Carole E.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
                                                  34;
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     Length 5179;
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                                                Indels
                                                                                                                                                                                   -----PRPLDRESPGVENKLIPSVGSPASSTPLPPDGT-----
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                                                                                                                                                                                                                                                                                                             65;
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Best Local Similarity 25.6%; Pred. No. 0.24;
Matches 41; Conservative 20; Mismatches 65;
Query Match 14.6%; Score 150; DB 10; Best Local Similarity 25.6%; Pred. No. 0.24; Matches 41; Conservative 20; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1068, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-10-078-547-24
; Sequence 24, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
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60 PPIPAPAPK-PAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAV-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TPVSQGSNSSSADPK-----APPPPPVSSGEPPTLGENPDGLSQEQLEHR- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 TPQLPSRSGVDSPRSGPRPPLPPDRPSAGAPPPPPSTSIRNGFQDSP---CEDEWESRF 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 NNK-----TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNS-----SQNTRL-QPT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.5%; Score 149; DB 14; Length 507; Best Local Similarity 26.9%; Pred. No. 0.027; Matches 61; Conservative 25; Mismatches 83; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ERSLQTLRDIQRMLFPDEKEFTGA---QSGGPQQNP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translated WIP ORF No. US20020199211A1 3
APPLICANT: Narayanaswamy Ramesh
APPLICANT: Miguel A. de la Fuente
APPLICANT: Ines M. Anton
APPLICANT: Ines M. Anton
APPLICANT: Raif S. Geha
IIILE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-005
CURRENT APPLICATION NUMBER: US/10/078,547
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/599,287
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1997-12-23
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 507
TYPE: PRT
CREATIRE:
CREANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
CTHER INFORMATION:
US-10-078-547-24
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Search completed: October 15, 2003, 10:50:59 Job time: 83.2802 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 46.0467 Seconds
(without alignments)
405.170 Million cell updates/sec October 15, 2003, 10:27:32 Run on:

US-09-915-543-15_COPY_199_392 1028 1 TIVSFHIQNISNNKTERSTA......LFPDEKEFTGAQSGGPQQNP 194 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

0 2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hybothetical prote	prot	QU.	_	-aldrich	_=		Ω	hypothetical prote	extensin-like prot	extensin - Volvox	Н	hypothetical prote	proline-rich prote	extensin-like prot	salivary proline-r		μ	proline-rich prote		pistil extensin-li	unknown protein [i	prpL2 protein - hu	pro	C N	hypothetical prote	pistil extensin-li	hypothetical prote	4
SUMMARIES		\$50755	T49801	vo	ന	00	18	B56708	75	0	σ	S22697	S16748	T04455	T05441	D85257	æ	S	A43932	D29149	T32711	JQ1696	G86441	S52796	B86369	OZZQBK	T34279	0047	Н	B24264
	gth DB	ŀ						815 2																						
dю	Query Match Length	7.3	6.4	٣.	5.8	5.8	5.8 1	15.7	5.6	5.4	5.4	5.3	5.2	5.0	4.8	4.8	4.6	4.6	4.6 3	5.5	4.5	4.5	.5	4.4	4.4	4.3	4.3	4.3	4.3	14.2
	Score	77	68	67	62	162.5	62	161.5	_	28	158.5	57	1	154.5	22	27	20	20	150	149	149	149		ထ	48	147	٦	46	146.5	146
	Result	H	7	e	4	5	9	7	ω .	on.	10	11	12	13	14	15	16	17	18	19	20	7.7	22	23	24	25	26	27	28	29

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S51939	A86335	S22373	S21961	A44358	T09024	F86387	T38236	\$76953	\$51342	A34418	D41727	I84718	S19560	OZZOMB
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439	1137	260	534	542	577	760	1611	535	817	446	448	520	300	332
14.2	14.2	14.2	14.1	14.1	14.1	14,1	14.1	14.0	14.0	14.0	14.0	14.0	13.9	13.9
146	146	145.5	145	144.5	144.5	144.5	144.5	144	144	143.5	143.5	143.5	143	143
30	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

Har

RESULT 2
149801
hypothetical protein B11B22.30 [imported] - Neurospora crassa
C; Species: Neurospora crassa
C; Species: Neurospora crassa
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Accession: T49801
R; Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Rcession: T49801
A; Accession: T49801
A; Status: preliminary
A; Molecule type: DNA
A; Cross references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.30
A; Experimental source: BAC clone B11B22; strain OR74A
C; Genetics:
A; Gene: NCSP:B11B22.30
A; Map position: 6
A; Introns: 75/3; 190/1; 449/3

RESULT 4 743556 Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000 C; Accession: T43556 R; Zankel, T.C.; Ow, D.W. Submitted to the EMBL Data Library, December 1997 A; Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces pomi A; Reference number: 222575 A; Accession: T43556 A; Accession: T4356 A; Accession:	Query Match 15.8%; Score 162.5; DB 2; Length 574; Best Local Similarity 30.9%; Pred. No. 0.017; Indels 27; Gaps 7; Matches 50; Conservative 21; Mismatches 64; Indels 27; Gaps 7; QY 7 IQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSQNT 54 1 1 1 1 1 1 1 1 1 1	RESULT 5 T38819 wiskott-aldrich syndrome protein homolog 1 - fission yeast (Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C; Accession: T38819 R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. Submitted to the EMBL Data Library, September 1997 A; Reference number: Z21813 A; Reference number: Z21813 A; Accession: T38819 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-574 <con> A; Residues: 1-574 <con> A; Residues: 1-574 <con> A; Experimental source: strain 972h-; cosmid c4F10 C; Genetimental source: strain 972h-; cosmid c4F10 C; Genetimental source: wspl: SPDR:SPAC4F10 15c</con></con></con>	Match 72/2 50 275 275 275 275 335 395 395
Query Match 16.4%; Score 168.5; DB 2; Length 876; Best Local Similarity 30.1%; Pred. No. 0.012; 61; Indels 61; Gaps 10; Matches 63; Conservative 24; Mismatches 61; Indels 61; Gaps 10; QY 3 VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQ 57 I 77 VSLNDNSTIGDKTGNPEKSLDTAPSSTKKLSISSIASALPAMPWSPSATDEAV 229 QY 58 PTPPIPAPAPRPRAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVT 117 I 59 VSPRAAAAAAAPPRPLOTERSPGVENKLIPSVGSPASSTPLGFDGTGPNSTPNNRAVT 117 I 1	RESULT 3 A46302 PTB-associated splicing factor, long form - human N;Alternate names: myoblast cell surface antigen 24.1D5; polypyrimidine tract-binding pr C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999 C;Accession: A46302; A43557; S29995 R;Patton, J.G.; Porro, E.B.; Galceran, J.; Tempst, P.; Nadal-Ginard, B. Genes Dev, 7, 393-406, 1993 A;Title: Cloning and characterization of PSF, a novel pre-mRNA splicing factor. A;Reference number: A46302; MUID:93194059; PMID:8449401 A;Accession: A46302 A;Molecule type: mRNA A;Residues: 1-707 <pat> A;Cross-references: EMBL:X70944; NID:938457; PIDN:CAA50283.1; PID:938458</pat>	A; Note: sequence extracted from NCBI backbone (NCBIP:127206) R; Gower, H.J.; Moore, S.E.; Dickson, G.; Elsom, V.L.; Nayak, R.; Walsh, F.S. Development 105, 723-731, 1989 A; Title: Cloning and characterization of a myoblast cell surface antigen defined by 24.1 A; Reference number: A43557; MUID:90091812; PMID:2480877 A; Reference number: A43557 A; Rolecule type: mRNA A; Residues: 312-707 <gow> A; Residues: 312-707 <gow> A; Residues: 312-707 <gow> A; Cross-references: GB:X16850; NID:923711; PIDN:CAA34747.1; PID:923712 C; Genetics: A; Gene GDB:SFPQ; PSF A; Cross-references: GDB:138275 A; Map position: 4q-4q C; Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein c; Superfamily: unassigned ribonucleoprotein repeat homology <rrmi> F; 298-359/Domain: ribonucleoprotein repeat homology <rrmi> F; 372-438/Domain: ribonucleoprotein repeat homology <rrmi></rrmi></rrmi></rrmi></gow></gow></gow>	Ouery Match Duest Local Similarity 40.0%; Pred. No. 0.011; Best Local Similarity 40.0%; Pred. No. 0.011; Matches 54; Conservative 5; Mismatches 47; Indels 29; Gaps 8; QY 30 RNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPARKPAAPPRPLDRESPGY 83 :

ين يم

R1

7.

22;

Length 839; Indels 5

Gaps

17;

Length 351;

118

RESULT 10

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RESULT

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Fybrian Protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C; Accession: F75518
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID: 20036896; PMID: 10567266
A; Accession: F75518
A; Status: preliminary
A; Molecule type: DNA
A; References: GB: AE001904; GB: AE000513; NID: 96458129; PIDN: AAF10038.1; PID: 964
A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C; Species: Chlamydomonas eugametos
C; Species: Chlamydomonas eugametos
C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C; Accession: S50754
R; Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Har Plant Mol. Biol. 26, 947-960, 1994
A; Title: Domain conservation in several volvocalean cell wall proteins.
A; Reference number: S50754; MUID:95093034; PMID:8000007
A; Accession: S50754
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-351 < WOE>
A; Cross-references: EMBL:L29028; NID:9530877; PIDN:AAB53954.1; PID:9530878
                                                                                                                                                                                                                                                                                                                                                                       GB:AE000513; NID:g6458129; PIDN:AAF10038.1; PID:g64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
C;Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 PKP-LPQQPPAPANQDQNSSQNTRLQP---TPPIPAPA---PKPAAP-PRPLDRESPGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 NKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGS-NSSSADPKAPPPPVSSGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 NISNNKTERSTAPLNTQ----ISALRNDPKPLPQQPPAPANQDQNS----SQNTRLQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.6%; Score 160; DB 2; L
Best Local Similarity 31.3%; Pred. No. 0.033;
Matches 52; Conservative 13; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 158.5; DB 2; 30.9%; Pred. No. 0.017; iive 15; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 GTAASSPESASPVTVTPRGET
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Best Local S
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C. Species: Homo sapinat regulated nimes.

C. Species: Homo sapinat regulated (man)

C. Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1999

C. Accession: B56708

R; Zhou, G.; Bao, Z.Q.; Dixon, J.E.

J. Biol. Chem. 270, 12665-12669, 1995

A; Title: Components of a new human protein kinase signal transduction pathway.

A; Reference number: A56708; MUID: 95279403; PMID: 7759517

A; Residues: 1-815 < ZHO>

A; Residues: 1-815 < ZHO>

A; Residues: 1-815 < ZHO>

A; Cross-references: GB: U25278; NID: 9837260; PIDN: AAA81381.1; PID: 9837261

C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homology < KIN>

F; 52-315/Domain: protein kinase homology < KIN>

F; 60-68/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                           chick
               RESULT 6
T18535
high molecular mass nuclear antigen - chicken (fragment)
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T18535
R; Shimada, K.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A; Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of c]
A; Reference number: Z18955; MUID:9803440; PMID:9365273
A; Reference number: Z18955; MUID:9803440; PMID:9365273
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1151 <SHI>A; Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 PKPLPQQPPAPANQDQNSSQNTRLQPTP-PIPAPAPKPAAPPRP-----LDRESPGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP---PPPPVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 PKWVPIGGAP-----PPPGTEP-----TPPSKPTDGADAAPKASAELTSPPPASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LPPDGT
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Pred. No. 0.027;
7; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 162.5; DB 2;
; Pred. No. 0.033;
12; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal-regulated kinase 5 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 EPPTLGENPDGLSQEQ 157
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Best Local Similarity 32.1%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.8%;
Best Local Similarity 33.1%;
Matches 45; Conservative 1
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hypothetical protein F4D11.90 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 04-Mar-2000
C; Accession: T04455
R; Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998
A; Reference number: Z15360
A; Rocession: T04455
A; Rocession: T04455
A; Residues: 1-731 < ABEV.
A; Rosidues: 
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C; Accession: T05441
R; Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schus submitted to the Protein Sequence Database, November 1998
A; Reference number: 215416
A; Accession: T05441
A; Molecule type: DNA
A; Residues: 1-379 <BEV>
A; Residues: 1-379 <BEV>
A; Residues: 1-379 <BEV>
A; Experimental source: cultivar Columbia; BAC clone F7K2
C; Genetics:
A; Map position: 4
             characterization of a proline-rich gene expressed specifi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSPKPGPSPSPPKPPPSPAPKPVP-----PPSPSPKPSPKPPAPSPKP-SPPKPP 111
                                                                                                                                                                                                                                                                                                                                                                                                                         ----SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPP 144
                                                                                                                                                                                                                                                                                                           33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVG
                                                                                                                                                                                                                                                                                                                                                      15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPK--PAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- PPDGTGPNST-PNNRAVTPVSQG-
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A;Description: Cloning and characterization of a proline
A;Reference number: S16748
A;Accession: S16748
A;Molecule type: mRNA
A;Residues: 1-449 <ROB>
A;Cross-references: EMBL:X60376; NID:g22596; PID:g22597
                                                                                                                                                                                                     Score 156; DB 2; I
Pred. No. 0.03;
9; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.0%; Score 154.5; DE Best Local Similarity 27.6%; Pred. No. 0.06; Matches 47; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRPLDRESPGVENKLIPSVGSPASSTPL----
                                                                                                                                                                                                   Query Match 15.2%;
Best Local Similarity 33.3%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           93
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C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C:Accession: S16748
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, submitted to the EMBL Data Library, August 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 PPPPVKSPPPPAPVSSPPPPVKS---PPPPAPVSSPPPVKSPPPAPISSPPPVKSPP 1077
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                                           C; Species: Zea may: maize)
C; Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C; Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C; Accession: 849915
R; Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
submitted to the EMBL Data Library, June 1994
A; Description: Pex genes: pollen-specific genes with extensin-like domains.
A; Reference number: 849915
A; Reference number: 849915
A; Accession: 849915
A; Accession: 849915
A; Accession: By Pellminary
A; Molecule type: DNA
A; Residues: 1-1188 < RUB>
A; Cross-references: EMBL: 234465; NID:g600117; PIDN:CAA84230.1; PID:g600118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence_revision 04-Dec-1992 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRES
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in
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; Pred. No. 0.026;
11; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 158.5; DB 2;
; Pred. No. 0.057;
17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P---PRSSPSPPPWVSPPPPPRASPPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .; Wenzl, S.; Sumper, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 49; Conserv
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                       extensin-like
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extensin-like protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C; Accession: D85257
R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID: 20083488; PMID: 10617198
A; Accession: D85257
A; Status: preliminary
A; Molecule type: DNA
A; Residence: GB:NC_001268; NID: 97269093; PIDN: CAB79202.1; GSPDB:GN00140
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 4
C; Superfamily: hydroxyproline-rich glycoprotein
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                                                                                                                                                                                                                                        SVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPPVSSGEPPTLGEN 149
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                                                                                                                                                                                                                                                                       33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPI---PAPAPKPAAPPRPLDRESPGVENKLIP 89
                                                                                                                                                                                 33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPI---PAPAPKPAAPPRPLDRESPGVENKLIP 89
                                                                                                               Gaps
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                                                                 Length 379;
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                                                             Query Match 14.8%; Score 152.5; DB 2; Best Local Similarity 31.8%; Pred. No. 0.041; Matches 41; Conservative 12; Mismatches 45;
                       hydroxyproline-rich glycoprotein
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A; Note: F7K2.50
C; Superfamily:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 15, 2003, 10:27:32; Search time 23.4008 Seconds (without alignments) 389.867 Million cell updates/sec

915-543-15_COPY_199_392 -60-sn

1028 1 TIVSFHIQNISNNKTERSTA.....LFPDEKEFTGAQSGGPQQNP 194 Title: Perfect score: Sequence:

62 10.0 , Gapext 0.5 BLOSUM Gapop Scoring table:

seqs, 47026705 residues 127863 Searched:

Total number of hits satisfying chosen parameters:

0 2000000000 Minimum DB seq length: Maximum DB seq length:

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 10

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	HIMAN	ALCECO NAMIN	013164 homo	Q9fpq6 chlam	E Q03173 1	P40603 brass	043516 homo	P02812 homo	P28702 homo	Q02817 homo	Q03211 nicot	LABA P23093	RATH P40602	RAT 09wv48	LABE P06915	HICK Q04584	P74745	FEAST	P28704 mus	MOUSE P05143 mus	Snm 62820 Mns	005860	P10162	P24152	000401	P13983 nico	099583	E Q9wvs8 mus	P93329 medi	095107		
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P10220 herpes simp P10161 homo sapien	PO5142 mus musculu	Ol0341 orgyia pseu	P03330 simian sarc	083384 treponema p	P49743 rattus norv	060610 homo sapien	002626 caenorhabdi	P48634 homo sapien	Q12446 saccharomyc	OB8935 mus musculu
TEGU_HSV11 PRPM_HUMAN	PRP2_MOUSE	Y091_NPVOP	GAG_SMSAV	Y369_TREPA	RXRB_RAT	DIA1_HUMAN	AEX3_CAEEL	BAT2_HUMAN	LA17_YEAST	SYN1_MOUSE
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13,5	13,	13	13	Ξ	H	H	H	H	-1	H
138.5 13.5 137.5 13.4	17	-1		, ,		• •	' '	'	• •	` '

ALIGNMENTS

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malignancies.
CAUTION: It is uncertain whether Met-1 or Met-27 is the initiator.
CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=1952490; PubMed=11955446;
Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.;
Murone M., Zuellig S., Basler K.;
Mut/wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";
Cell 109:47-60(2002).
-!- FUNCTION: Involved in signal transduction through the wnt pathway.
-!- SUBCILLULAR LOCATION: Nuclear (Probable).
-!- SUBCILLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: Detected at low levels in thymus, prostate, testis, ovary and small intestine, and at lower levels in spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: Involved in a t(1;14)(q21;q32) chromosomal translocation found in a patient with precusor B-cell acute lymphoblastic leukemia (ALL). This translocation leaves the coding region intact, but may have pathogenic effects due to alterations in the expression level of BCL9. Several cases of translocations within the 3' untranslated region of BCL9 have been found in B-cell
                                                                                                                                                                                                                                                                                                                        Dyer.M.J.S.;
"Molecular cloning of translocation t(1;14)(q21;q32) defines a novel gene (BCL9) at chromosome 1q21.";
Blood 91:1873-1881(1998).
                                                                                                                                                                                                                                             TISSUE=Fetal brain;
MEDLINE=98158621; PubMed=9490669;
Willis T.G., Zalcberg I.R., Coignet L.J.A., Wlodarska I., Stul M.,
Jadayel D.M., Bastard C., Treleaven J.G., Catovsky D., Silva M.L.M.,
                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
B-cell lymphoma 9 protein (Bcl-9) (Legless homolog).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon and blood
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
BCL9_HUMAN
                                                                                                                                                                                                                                                                                                      Jadayel D
Dyer M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION
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40:26 2003

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120
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Zhang W.-W., Zhang L.-X., Busch R.K., Farres J., Busch H.;
"Purification and characterization of a DNA-binding heterodimer of 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2480877;
e S.E., Dickson G., Elsom V.L., Nayak R., Walsh F.S.;
racterization of a myoblast cell surface antigen
5 monoclonal antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 707 AA.

P23246; P30808;
01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
58-FICTOR (PSF) (DNA-binding P52/P100 complex, 100 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patton J.G., Porro E.B., Galceran J., Tempst P., Nadal-Ginard B., "Cloning and characterization of PSF, a novel pre-mRNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING.
TISSUE=Fetal brain;
MEDLINE=93194059; PubMed=8449401;
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                        Length 1426;
                                                                                                     Thromosomal translocation; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                       POLY-PRO 3.
MW; A240A487716B7F1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Score 1024; DB 1;
Pred. No. 4.3e-45;
0; Mismatches 1;
                                                                                                                                                                                 CINNB1-BINDING.
POLY-PRO 1.
                                                                                                                                                                                                                                  POLY-PRO 2.
POLY-ALA.
                                                                                                                                                          PRO-RICH
73942.1; ALT_FRAME
                                                                            oncogenesis; TAS
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267-272(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              letal muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                               hway.
1378
377
335
517
903
                Genew, HGNC:1008; B
MIN; 602597; -.
GO; GO:0007048; P:0
Nuclear protein; Ch
Wnt signaling pathw
DOMAIN 231 1
DOMAIN 347
DOMAIN 514
DOMAIN 514
DOMAIN 900
DOMAIN 970
SEQUENCE 1426 AA;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 193; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fetal skel
MEDLINE-90091812;
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MEDLINE=93176127
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Biochem. J. 290:
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EMBL; Y13620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 RNDPKPLPQQPPAPANQDQN--SSQNTRLQPTPPIPAPAPKP----AAPPRPLDRESPGV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTERFGGGGAGPVGGGGRGMGPGTPAGYGRGREFYEGPNK
KPRF -> VRMIDVG (in isoform Short).
/FTId=VSP_005855.
G -> R (IN REF. 3).
6 DBD5EA95E235847 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
FUNCTION: ESSENTIAL PRE-MRNA SPLICING FACTOR REQUIRED EARLY IN SPLICEOSOME FORMATION. BINDS TO THE MAMMALIAN POLYPRIMIDINE TRACTS. FORMS A COMPLEX WITH THE POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB). SEEMS TO ALSO BIND DNA. SUBUNIT: HETEROTETRAMER OF TWO 52 KDA AND TWO 100 KDA SUBUNITS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 1.
Nuclear protein; RNA-binding; DNA-binding; mRNA splicing; Repeat;
Alternative splicing.
                                                                                                                                 Name=Short;
Name=Short;
Isold=P23246-1; Sequence=VSP_005855;
Isold=P23246-2; Sequence=VSP_005855;
SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE MYOBLAST CELL SURFACE ANTIGEN 24.1D5 AND A POSSIBLE MEMBRANE-BOUND PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.3%; Score 167.5; DB 1; Length 707; 40.0%; Pred. No. 0.031; tive 5; Mismatches 47; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 605199; -.
GO; GO:0008248; F:pre-mRNA splicing factor activity; TAS.
GO; GO:0006371; P:mRNA splicing; TAS.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
3 x 3 AA REPEATS OF 1
                                                                                           Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLN/GLU/PRO-RICH
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POLY-PRO.
POLY-PRO.
POLY-ARG.
POLY-ARG.
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                    EMBL; X70944; CAA50283.1; -.
EMBL; X16850; CAA34747.1; -.
PIR; A46302; A46302.
HSSP; P11940; 1CVJ.
SWISS-2DPAGE; P23246; HUMAN.
Genew; HGNC:10774; SFPQ.
GK; P23246; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
76149 MW;
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272
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707 AA;
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hes 54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95374539; Pubmed=7646528;

A Lee J.-D. Ulevitch R.J., Han J.;

Lee J.-D. Ulevitch R.J., Han J.;

Thrimary structure of BMK1: a new mammalian map kinase.";

Biochem. Biophys. Res. Commun. 213:715-724(1995).

-!- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE ANOTHER AND NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.

-!- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE ANOTHER AND COMMINER REGULATION: Activated by tyrosine and threonine phosphorylation (By similarity).

-!- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. ABUNDANT IN HEART, PLACENTA, LUNG, KIDNEY AND SKELETAL MUSCLE. NOT DETECTABLE IN LIVER.

-!- DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.

-!- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY ROLE, IS ABSENT.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
     --PDGTGPNSTPN-NRAVTPVSQGSNSSSADP 130
                                                                                                                                                                                                               35, Created)
35, Last sequence update)
40, Last annotation update)
1 protein kinase 7 (EC 2.7.1.-) (Extracellular signal-5) (ERK-5) (ERK-1) (BMK1 kinase).
                                     --SAPP
                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              , Dixon J.E.;
new human protein kinase signal transduction
                     815 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP kinase activity;
signal transduction;
77; MAP_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:12665-12669(1995)
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       n;
PubMed=7759517;
, Dixon J.E.;
 EN--KLIPSVGS--PASSTPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A82931.1; -.
A82932.1; -.
A82932.1; -.
                                                               KAPPPPPVSSGEPPT 145
|||| | || | | |
GAPPPTPPSSGVPTT 177
                                                                                                                                                                                    ANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPK7
                                                                                                                                             RESULT 3
MK07_HUMAN
ID MK07_HUMAN STAN
AC Q13164; Q16634;
DT 01-NOV-1997 (Rel. 3
DT 01-NOV-1997 (Rel. 3
DT 16-OCT-2001 (Rel. 4
DE Mitogen-activated p
DE regulated kinase 5)
GN MAPK7 OR PRKM7 OR E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U25278; AAA81:
EMBL; U29725; AAA82:
EMBL; U29726; AAA82:
EMBL; U29727; AAA82:
PIR; B56708; B56708
HSSP; P24941; 1HCL.
Genew; HGNC:6880; M.
MIM; 602521; -.
GO; GO:0004707; F:M.
GO; GO:0007165; P:S:
InterPro; IPR003527
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Fetal brain, MEDLINE=95279403; I Zhou G., Bao Z.Q., "Components of a ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=95374539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ";
Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathway.";
J. Biol. C
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84
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InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; PONSTER PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; PONSTER PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; PONSTER PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; PONSTER PROSITE; PS00108; PS0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 RPAAPALTSVPAPAPAPTPTPTPVQPTSPPPGPLAQPTGPQPQSAGSTSGPVPQPACPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (ACTIVATES THE KINASE)

(BY SIMILARITY).

PHOSPHORYLATION (ACTIVATES THE KINASE)

(BY SIMILARITY).

AREGRTPHRCLCS -> GPVKVEPAHTAASVA (IN

REF. 2).

L -> V (IN REF. 2).
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٦.
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09FP06; Q03927;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation
encoding cell wall hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> V (IN REF. 2).
379AD69803207CCF CRC64;
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MEDLINE=21159092; PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 161.5; DB 1;
Pred. No. 0.069;
7; Mismatches 64;
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PRO-RICH 1.
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PRO-RICH 2
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32.1%;
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Matches 54; Conservative
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Gertler F.B., Niebuhr K., Reinhard M., Wehland J., Soriano P.;
"Mena, a relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENANH MOUSE STANDARD; PRT; 802 AA.
003173; P70430; P70431; P70432; P70433;
01-OCT-1996 (Rel. 34, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Enabled protein homolog (NPC derived proline-rich protein 1) (NDPP-1).
ENAH OR MENA OR NDPP1.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 87:7355-7359(1990).
or component of the outer cell wall W6 (crystalline)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
6A584A90465502F5 CRC64;
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                                                                      SUBUNIT: Associates with GP2 and GP3, PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M58496; AAA69706.1; ALT_SEQ. GlycoSuiteDB; Q9FPQ6; ...
InterPro; IPR002965; P_rich_extensn. InterPro; IPR003882; Pistil_extensin. PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Repeat; Signal.
SIGNAL 1 29 PO.
CHAIN 30 555 VED
DOMAIN 259 279 PO.
CARBOHYD 399 399 N-1
CARBOHYD 455 455 N-1
CARBOHYD 493 493 N-1
SEQUENCE 555 AA; 54219 MW;
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32.8%;
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Best Local Similarity
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"Identification of
central nervous sys
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      Proc. Natl. Acad.
                                                                                                PTM: N-91ycos
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MEDLINE=93041923;
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MEDLINE=97015079;
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                                 Prunction, AND SUBUNIT.

MEDLINE=99166867; PubMed=10069337;
A Lanier L.M., Gates M.A., Witke W., Menzies A.S., Wehman A.M.,
A Lanier L.M., Gates M.A., Witke W., Menzies A.S., Wehman A.M.,
A Macklis J.D., Kwiatkowski D., Soriano P., Gertler F.B.;
Then is required for neurulation and commissure formation.*;

The contint of the formation of F-actin rich outgrowths in fibroblasts. Required for neurulation and commissure formation.

The contint of the formation of F-actin rich outgrowths in fibroblasts. Required for neurulation and commissure formation.

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Name=2; Synonyms=Mena;
Isold=003173-3; Sequence=VSP_007259, VSP_007260;
Name=3; Synonyms=Mena+;
Isold=003173-4; Sequence=VSP_007259;
Name=4; Synonyms=Mena++;
Isold=003173-5; Sequence=VSP_007257, VSP_007258;
TISOLS SPECIFICITY: IN THE HEART AND TESTIS AND LESS SO IN THE LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS AND BRAIN.
SIMILARITY: Contains 1 WH1 domain.
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/FTId=VSP_007259.
Missing (in isoform 2).
/FTId=VSP_007260.
592BB975EE20F77F CRC64;
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/FTId=VSP_007256.
Missing (in isoform 4).
/FTId=VSP_007257.
CIFC -> VFYL (in isoform 4).
/FTId=VSP_007258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enesis; Alternative splicing.
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EMBL; U72520; AAC52863.1; -...
EMBL; U72521; AAC52864.1; -...
EMBL; U72522; AAC52865.1; -...
EMBL; U72523; AAC52866.1; -...
PIR; S27200; S27200.
MGD; MGI:108360; Enah.
InterPro; IPR001960; WH1.
Pfam; PF00568; WH1; 1...
SMART; SM00461; WH1; 1...
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DOMAIN 1 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).
                                                                                 407
                                                                                                                                                                             SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                SPVPQMPPSPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPPPPPPPPPPPPLAS
                                                                                                                                                           ----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV-
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eudicots; Rosidae;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS. STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING VELOPMENT, HIGHER EXPRESSION IS FOUND DURING TOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
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                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment)
APG OR CEX.
                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.W., Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sporophytic expression of an anther-specific ana gene."; 0(1993).
    Length 802;
                                                                                                                                                                                                               ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                             Indels
                                                                                                                                                                                                                               APG OR CEX.

Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eucosids II; Brassicales; Brassicaceae; Brassica.
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                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9EFB6A3AB28EEA15
     DB 1;
                                                        --QISALRNDP-
               0.1;
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15.4%; Score 158; DF 26.3%; Pred. No. 0.1; ative 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        er G.D., Blundell R.P.,
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                             rvative
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  Query Match
Best Local Similarity
Matches 59; Conserv
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InterPro; IPR001087
InterPro; IPR0013882
Pfam; PF00657; Lipe
PROSITE; PS01098; I
NON_TER 132
ACT_SITE 132
ACT_SITE 428
SEQUENCE 449 AA;
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Arabidopsis thaliar
Plant J. 3:111-120
-!- TISSUE SPECIFIC
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MICROSPORE MITH
MATURATION.
SIMILARITY: BE
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P40603;
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Length 449;

Score 156; DB 1; Pred. No. 0.079;

15.2%; 33.3%;

Query Match Best Local Similarity

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043516; 015220; 09UNP1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Wiskott-Aldrich syndrome protein interacting protein (WASP interacting
                                                                                                                                              PSPKPGPSPSPPKPPSPAPKPVP-----PPSPSPKPSPPKPPAPSPKP-SPPKPP 111
                                33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVG
                                                                 2 PKPQPKPPPKPQPKPPPAPTPSPCPPQPPKPQPKPPPAPTPSPCPPQPFKPQPKPPPAPG
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98070810; PubMed=9405671;
Ramesh N., Anton I.M., Hartwig J.H., Geha R.S.;
"WIP, a protein associated with Wiskott-Aldrich syndrome protein, induces actin polymerization and redistribution in lymphoid cells.";
Proc. Natl. Acad. Sci. U.S.A. 94:14671-14676(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew, HGNC:12736; WASPIP.
MIM, 602357; -.
GO; GO:0015629; C:actin cytoskeleton; TAS.
GO; GO:0003779; F:actin binding activity; TAS.
GO; GO:0008154; F:profilin binding activity; TAS.
GO; GO:0008154; P:actin polymerization and/or depolymerization; TAS.
GO; GO:0006461; P:protein complex assembly; TAS.
InterPro; IPR003124; WH2.
Pfam; PF02205; WH2; 1.
                                                                                                           ----SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interacting protein.";
J. Immunol. 162:5019-5024(1999).
-!-FUNCTION: MAY HAVE DIRECT ACTIVITY ON THE ACTIN CYTOSKELETON.
INDUCES ACTIN POLYMERIZATION AND REDISTRIBUTION.
-!- SUBUNIT: BINDS TO WASP, PROFILIN AND ACTIN.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PERIPHERAL BLOOD MONONUCLEAR CELLS, SPLEEN, PLACENTA, SMALL INTESTIN, COLON, THYMUS. LOWER EXPRESSION IN OVARY, HEART, BRAIN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 192-503 FROM N.A., AND VARIANT ALA-495.
MEDLINE=99218549; PubMed=10202051;
Stewart D.M., Tian L., Nelson D.L.;
"Mutations that cause the Wiskott-Aldrich syndrome impair the interaction of Wiskott-Aldrich syndrome protein (WASP) with WASP
     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreideweiss S., Delany-Heiken P., Nordheim A., Ruhlmann
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; F
Catarrhini; Hominidae;
  57;
  Mismatches
 6
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EMBL; AF106062; AAD45972.1; -.
EMBL; X86019; CAA60014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                             protein) (PRPL-2 protein).
WASPIP OR WIP,
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
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TISSUE=Tonsil;
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39;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNSSSADPK----APPPPPPVSSGEPPTLGENPDGLSQEQLEHR-- 161
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                                                                                                                                                                                                                                                                                                                 PHRPHLR -> SSQAPPP (IN REF. 3).
P -> PV (IN REF. 2).
GSNRRERGGPPLPPIPR -> EYFCQGF (IN REF. 2)
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein precursor (Clone CP7) [Contains: Basic peptide P-F] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saitoh E., Isemura S., Sanada K.; "Complete amino acid sequence of a basic proline-rich peptide, P-F, from human parotid saliva."; J. Biochem. 93:883-888(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85289325; PubMed=2993301;
MEDLINE=85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
"Differential RNA splicing and post-translational cleavages in the
human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 151.5; DB 1; Length 503; 26.5%; Pred. No. 0.15; Live 25; Mismatches 84; Indels 57
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G -> A.
                                Polymorphism, POLY-PRO.
                                                                                 GLY-RICH
                                                                                                                                    PRO-RICH
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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96
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488
                            Repeat;
          WH2;
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MEDLINE=83265674; Pu
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60; Conserv
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Actin-binding; Re
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DOMAIN 241
DOMAIN 241
BEPEAT 352
REPEAT 374
REPEAT 410
SITE 45
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360
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P02812;
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CONFLICT
SEQUENCE
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105 GDNKSQGP-----PPPGKPQGPPPQGGSKSRSSRSPPGKPQGPPPQGGN----QPQGPPP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 NKPQGPPPPGKPQGPPPQGDNKSQSARSPPGKPQGPPPQGGNQPQGPPPPGKPQGPPPQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IPAPAPKPAAPPRP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 LDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification, cloning, and RXR identity of the HeLa cell factor with which RAR or TR heterodimerizes to bind target sequences efficiently.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92253386; PubMed=1315958;
Fleischhauer K., Park J.H., Disanto J.P., Marks M.S., Ozato K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of a full-length cDNA clone encoding a N-terminally variant form of the human retinoid X receptor beta."; Nucleic Acids Res. 20:1801-1801(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.6%; Score 150.5; DB 1; Length 251; Best Local Similarity 31.2%; Pred. No. 0.091; Matches 43; Conservative 9; Mismatches 61; Indels 25,
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MEDLINE~92127595; PubMed=1310259;
Leid M., Kastner P., Lyons R., Nakshatri H., Saunders M.,
Zacharewsi T., Chen J.Y., Staub A., Garnier J.M., Mader S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leid M., Kastner P., Lyons R., Nakshatri H., Saunders M., Zacharewsi T., Chen J.Y., Staub A., Garnier J.M., Mader S.
                                                                                                                                                                                                                                                                                                                                                                                                         24641 MW; D779F590C0EBF30B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 NDPK--PLPQQPPAPANQDQNSSQNTRLQPTPP-----
                                                                                                                                                                                                                                                 BASIC PEPTIDE P-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RXRB_HUMAN STANDARD; PRT; 533 AA. P28702; P28703; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
or send an email to license@isb-sib.ch).
                                                                                                                                                               Parotid gland, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93046692; PubMed=1330328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinoic acid receptor RXR-beta.
RXRB OR NR2B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 PP-VSSGEPPTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 PPGKPQGPPPQGGNKPQG 173
                                                   EMBL; K03208; AAA60189.1; -. PIR; E25372; PIHUPF. Genew; HGNC:9338; PRB2.
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134
251 AA;
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                                                                                                                                                                                                                                                                            REQUENCE FROM N.A.

RECURE-Brain;

RECURE-Brain;

RECURE-Brain;

RECURE-22388257; PubMed=12477932;

RECURE-22388257; PubMed=12477932;

RECURE-22388257; PubMed=12477932;

RECURE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

RA Distrchenko L., Marusina K., Farmer A.A., Rubin G.M., Bond L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Walen P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Brownstein B.S., Morey D.M., Scherer G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

ROCT. Human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

PEUCTION: INVOLVED IN RETINOIC ACID RESPONSE PATHWAY. BINDS 9-CIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Long;
IsoId=P28702-1; Sequence=Displayed;
Name=Short;
IsoId=P28702-2; Sequence=Not described;
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
                                                                          SEQUENCE FROM N.A.
Corella A., Vergara A., Paez G., de Miguel C., Encio I.;
Corella A., Vergara A., Paez G., de Miguel C., Encio I.;
"Molecular cloning and characterization of the human HRXRB gene and 5'
 H., Ueyama K., Maeda S., Sakou T., Harata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:retinoid-X receptor activity; TAS. F:transcription co-activator activity; TAS.
Numasawa T., Koga H., Ueyama K., Maeda S., Sakou T., Har
Leppert M., Inoue I.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           flanking region.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             SEQUENCE FROM N.A.
Tubby B.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC18599.1; -. CAA20239.1; -. AAH01167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X63522, CAA45087.1; -. M84820; AAA60293.1; -. AF065396; AAC18599.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '8; RXRB.
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EMBL; M84820; AAA
EMBL; AF065396; A
EMBL; AF120161; A
EMBL; AL031228; C
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82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPRAP----- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPRPLDRESP
InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001628; Zaf_C4steroid.

Pfam; PF00104; hormone_rec; 1.

Pfam; PF00105; zf-C4; 1.

R Pfam; PF00105; zf-C4; 1.

R PRINTS; PR00039; STRDHORMONER.

R PRINTS; PR00047; STROIDFINGER.

R PRODOM; PR000035; Zaf_C4steroid; 1.

R SMART; SM00399; Zaf_C4; 1.

R SMART; SM00399; Zaf_C4; 1.

R SMART; SM00399; Zaf_C4; 1.

R PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

R PROSITE; PS00031; NUCLEAR_RECEPTOR SPIICING; 3D-Structure.

T DOMAIN 205 270 NUCLEAR RECEPTOR-TYPE.

T ZN_FING 205 225 C4-TYPE.

T ZN_FING 205 225 C4-TYPE.

T DOMAIN 271 330 HINGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUC2_HUMAN STANDARD; PRT; 5179 AA.
002817; Q14878;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mucin 2 precursor (Intestinal mucin 2).
MUC2 OR SMUC.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 150.5; DB 1; Length 533;
; Pred. No. 0.17;
11; Mismatches 45; Indels 33
                                                                                                                                                                                                                                                                                                                                    LIGAND-BINDING (BY SIMILARITY).
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D0069FE93AC16A04 CRC64;
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MEDLINE=93016075; PubMed=1400449;
                                                                                                                                                                                                                                                                                                                                                                                        56921 MW;
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31.0%;
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domain.
                                                                                                                                                                                                                                                                                                                                                          MUCIN 2.
APPROXIMATE REPEATS
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                                                                                                                                                                                                                               C:secretory vesicle; T. 208; Cys_knot.
207; Cys_knot_C.
209; EGF_like.
319; TIL_Cysrich.
307; VWF_C.
46; VWF_D.
                                                                                                                                                                               EMBL; L21998; AAB5295.1; --
EMBL; M44027; AAA59875.1; --
EMBL; M44027; AAA59163.1; --
EMBL; M44027; AAA59163.1; --
EMBL; M49963; AA4392.1; --
EMBL; M49963; AAA59164.1; --
PIR; A49963; AAA35164.1; --
PIR; A49963; AAA35164.1; --
GO, GO:0005803; C:SECTECTY VESICLE;
InterPro; IPR006208; Cys_knot_C.
InterPro; IPR006209; EGF_like.
InterPro; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_C.
InterPro; IPR001846; VWF_C.
InterPro; IPR001846; VWF_C.
Pfam; PF00093; VWC; 1.
Pfam; PF00094; VWC; 2.
SMART; SM00216; VWD; 4.
SMART; SM00216; VWD; 4.
SMART; SM00216; VWD; 4.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS01208; VWFC_2; 2.
Glycoprotein; Repeat; Signal.
CHAIN 1401 1416 1.
REPEAT 1472 1432 3.
REPEAT 1472 1438 3.
REPEAT 1479 1494 7A.
REPEAT 1479 1494 7A.
REPEAT 1479 1494 7A.
REPEAT 1479 1494 7A.
REPEAT 1479 1495 1517 7B.
REPEAT 1557 1557 9A.
REPEAT 1573 1596 9B.
REPEAT 1573 1596 8B.
REPEAT 1573 1597 1612 100A.
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1487 PTTTTTTPPPTTTPSPPMTTPITP----PASTTTLPPTTTPSPPTTTTPPPTTTPSPP 1542
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L -> S (IN REF. 3).
L -> P (IN REF. 3).
M -> T (IN REF. 3).
G -> S (IN REF. 3).
G -> S (IN REF. 2).
W, BSCD7571FB9A5663 CRC64;
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(GLCNAC.
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; Pred. No. 1.3;
20; Mismatches
                                                                                                                      SIMILARITY.
SIMILARITY.
SIMILARITY.
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SEQUENCE FROM N.A.

STRAIN=cv. Petit Havana; TISSUE-Pistil;

MEDLINE=93005740; PubMed=1392607;

Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;

"Developmental expression of tobacco pistil-specific genes encoding novel extensin-like proteins.";

Plant Cell 4:1041-1051(1992).

-! TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).

-! DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN 4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..) (POTENTIAL).
51A495CC94017812 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%; Score 149; DB 1; 29.9%; Pred. No. 0.17;
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Mismatches
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PIR; JQ1696; JQ1696.
InterPro; IPR006041; Ole_el_ext.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003882; Pistil_extensin.
Pfam; PF01190; Pollen_Ole_e_I; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSN.
Structural protein; Signal; Repeat; Gly.
SIGNAL 1 23 PISTIL-SPEC DOMAIN 69 182 4 x 5 AA R1 REPEAT 76 80 2.
REPEAT 76 80 2.
REPEAT 76 80 3.
REPEAT 76 80 4.
CARBOHYD 310 310 N-LINKED (0 SEQUENCE 426 AA; 44278 MW; 51A495CC;
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PSPAAEPPIIAPFP 261
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P23093;
01-NOV-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLINATION
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Best Local Simi
Matches 40;
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ID CSP_P
AC P2309
DT 01-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 KNEKKNKIER-----NNKLK--QPPPPPPNPNDPPPPNPND------PPPPPNPNDPP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 APAPKPAAPPRPLDRESPGVENKLIPSVGSPA---SSTPLPPDGTGP----NSTPNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                              MEDLINE=90221834; PubMed=2183186;

Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;

"Nucleotide sequence of the Plasmodium berghei circumsporozoite

protein gene from the ANKA clone 2.34L.";

Nucleic Acids Res. 18:376-376(1990).

-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT

SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE

MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE

VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Circumsporozoite protein precursor (CS).
Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 147; DB 1; Length 347; 29.9%; Pred. No. 0.18;
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17 X 2 AA REPEATS
TSP TYPE-1.
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POTENTIAL.
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PIR; S07873; OZZQBK.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL.
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93
214
274
347 AA;
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ogis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Ogis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Alonso J., Alafaí H., Cheuk R.E., Chin C.W.,
Er E., Chan A., Chao Q., Chen H., Cheuk R.E., Chin C.W.,
M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
J.E., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
J.L., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
I., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Scher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
I., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
I., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,
Lasler T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
[.2 sequence differs from that shown due to erroneous
brediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vis R.W., Ecker J.R., Theologis A.;
still length cDNA clones (RAFLS) sequenced by the Salk/Stanford/PGEC).";
001) to the EMBL/GenBank/DDBJ databases.
FICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL
ANTHER, ONLY IN MALE FERTILE PLANTS.
L STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING EVELOPMENT. HIGHER EXPRESSION IS FOUND DURING ITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I. Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M. Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";
Nature 408:816-820(2000).
                                                                                                                                                                                                                                                              Draper J., Scott R., "Gametophytic expression of an anther-specific Arabidopsis thaliana gene."; Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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InterPro; IPR001087; Lipase_GDSL.
InterPro; IPR003882; Pistil_extensin.
Pfam; PF00657; Lipase_GDSL; 1.
PRINTS; PR01218; PSTLEXTENSIN.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J.,
White O., Alonso J., Altafi B., Arauj
Buehler E., Chan A., Chao Q., Chen H.
Chung M.K., Conn L., Conway A.B., Con
Dunn P., Etgu P., Feldblyum T.V., Fen
Gill J.E., Goldsmith A.D., Haas B., F
Hunter J.L., Jenkins J., Johnson-Hops
Kim C.J., Koo H.L., Kremenetskaia I.,
Langin-Hooper S., Lee A., Lee J.M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF79900.1; ALT_SEQ.
AAL24235.1; -.
                                                                                                                                                                                                    PubMed≈8401599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-200
-!- TISSUE SPECIFI
TYPES IN THE A
-!- DEVELOPMENTAL
MICROSPORE DEV
MARCHINE MICROSPORE MIT
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=94004980; Roberts M.R., Fost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=cv. Columbi
Shinozaki K., Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ref.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATURATION.
SIMILARITY:
CAUTION: Ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene model
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Signal.
Signal
CHAIN
ACT_SITE
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              HIIM BERRARE B
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93 PKPQPKPPPAPSPSPCPSPPFKPQPKPVPPACPPTPPKPQPKPAPPPPAPP 152
                                                                                                                                                                              33 PKPLPQQPPAPA-NQDQNSSQNTRLQPTPP-----IPAPAPKPAAPPRPLDRESPGVEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yao I., Hata Y., Hirao K., Deguchi M., Ide N., Takeuchi M., Takai Y.; "Synamon, a novel neuronal protein interacting with synapse-associated protein 90/postsynaptic density-95-associated protein."; J. Biol. Chem. 274:27463-27466(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GKAP/SAPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), AND INTERACTION WITH DLGAP1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 4), AND INTERACTION WITH DLGAPI. STRAIN-Sprague-Dawley;
MEDLINE=99360650; PubMed=10433268;
Naisbitt S., Kim E., Tu J.C., Xiao B., Sala C., Valtschanoff J., Weinberg R.J., Worley P.F., Sheng M.;
"Shank, a novel family of postsynaptic density proteins that binds to the NMDA receptor/PSD-95/GKAP complex and cortactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99436166; PubMed=10506216;
Lim S., Naisbitt S., Yoon J., Hwang J.I., Suh P.G., Sheng M., Kim E.;
"Characterization of the Shank family of synaptic proteins. Multiple
genes, alternative splicing, and differential expression in brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobaben S., Suedhof T.C., Stahl B.; "The G protein-coupled receptor CL1 interacts directly with proteins of the shank family."; J. Biol. Chem. 275:36204-36210(2000).
                                                                                                                                                                                                                                                                     86 KLIPSVGSPASST--PLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPP 137
                                                                                                                                                                                                                                                                                                                                                                      SHAL RAT STANDARD; PRT; 2167 AA. Q9WV48; Q9QZZ8; Q9WU13; Q9WUE8; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) SH3 and multiple ankyrin repeat domains protein 1 (Shank1) (GKAI interacting protein) (SPANK-1) (Synamon) (Somatostatin receptor interacting protein) (SSTR interacting protein) (SSTRIP).
                                                                                                        14.2%; Score 146; DB 1; Length 534; llarity 34.2%; Pred. No. 0.29; Conservative 10; Mismatches 45; Indels
 POTENTIAL.

S -> P (IN REF. 1).

E -> A (IN REF. 1).

E -> H (IN REF. 1).

A; BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; 4 AND
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                                                                                                                        Pred. No. 0.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. (ISOFORM 4).
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development.";
J. Biol. Chem. 274:29510-29518(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99419021; PubMed-10488079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=20549637; PubMed=10958799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
511 PC
77 S
141 E
325 E
58007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the NMDA receptor/PSD-95,
Neuron 23:569-582(1999).
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511
77
141
325
534 AA;
                                                                                                                          Local Similarity
Les 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
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  ACT_SITE
CONFLICT
                                   CONFLICT
                                                        CONFLICT
                                                                       SEQUENCE
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                   Qγ
     SETTES
                                                                                                                                                                               Qγ
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ISOId=Q9WV48-5; Sequence=VSP_006076, VSP_006077;
TISSUE SPECIFICITY: Expressed only in brain (neuropil of cortex, CA1 region hippocampus and molecular layer of cerebellum).
DEVELOPMENTAL STAGE: Expression increases from low levels at birth to high levels at 3-4 weeks before dropping slightly in adulthood. Expressed in the cortex and the molecular layer of the cerebellum at postnatal day 7. Isoform 2 expression does not change during developmment of both cortex and cerebellum. Isoform 4 expression decreases significantly during development of cortex but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shank family of scaffold proteins.";

Cell Sci. 113:1851-1856(2000).

FUNCTION: Seems to be an adapter protein in the postsynaptic density (PSD) of excitatory synapses that interconnects receptors of the postsynaptic membrane including NMDA-type and metabotropic glutamate receptors, and the actin-based cytoskeleton. May play a role in the structural and functional organization of the dendritic spine and synaptic junction. Overexpression promotes maturation of dendritic spines and the enlargement of spine heads via its ability to recruit Homer to postsynaptic sites, and
                                                                                                INTERACTION WITH HOMER-1, AND SUBCELLULAR LOCATION.

MEDLINE=99360651; PubMed=10433269;

Tu J.C., Xiao B., Naisbitt S., Yuan J.P., Petralia R.S., Brakeman P.,
Doan A., Aakalu V.K., Lanahan A.A., Sheng M., Worley P.F.;

"Coupling of mGluk/Homer and PSD-95 complexes by the Shank family of postsynaptic density proteins.";
Neuron 23:583-592(1999).
                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homomultimerize via its SAM domain. Interacts with
-1 and DLGAP1/GKAP. Is part of a complex with
nd DLGAP1/GKAP. Interacts with SSTR2 C-terminus via
                                                                                                                                                                                                                                                                                                                       the
                 M., Liu G., Sheng M.; and synaptic function by
                                                                                                                                                                                                                                       INTERACTION WITH SPTAN1.

MEDLINE=21523912; PubMed=11509555;

Bockers T.M., Mameza M.G., Kreutz M.R., Bockmann J., Weise C.,
Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.;

"Synaptic scaffolding proteins in rat brain. Ankyrin repeats of multidomain Shank protein family interact with the cytoskeletal protein alpha-fodrin.";

J. Biol. Chem. 276:40104-40112(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n (By similarity).
OCATION: Cytoplasmic; postsynaptic density of
s. Colocalizes with alpha-latrotoxin receptor
RODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09WV48-2; Sequence=VSP_006072, VSP_006073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tive splicing; Named isoforms=5;
itional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION.
MEDLINE=21389514; PubMed=11498055;
Sala C., Piech V., Wilson N.R., Passafaro "Regulation of dendritic spine morphology Shank and Homer.";
Neuron 31:115-130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9WV48-3; Sequence=VSP_006074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yms=A;
8-4; Sequence=VSP_006075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
IsoId=Q9WV48-1; Sequence=Displayed;
 PubMed=10551867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10806096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: May h
SPTAN1, Homer-
DLG4/PSD-95 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20267867;
Sheng M., Kim E.;
"The Shank family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9WV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the PDZ domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alterna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment=Add
 MEDLINE=20020275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The Shar
J. Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVIEW
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SHANK FAMILY

ELONGS TO THE

SIMILARITY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2).

/FTIG=VSP_006072.
SQEGRQESRSDKARRLFRHYTVGSYDSFDAPSLIDGIDSG
-> MALSAVGGPGGGALPQPPPALSSSWPALGPRRRSVWY
IY (in isoform 2).
/FTIG=VSP_006073.
Missing (in isoform 3).
/FTIG=VSP_006074.
Missing (in isoform 4).
/FTIG=VSP_006075.
LSEDSQTSLLSRPS -> QYRIVVKSSDFGDF (in isoform 5).
/FTIG=VSP_006075.
LSEDSQTSLLSRPS -> QYRIVVKSSDFGDF (in isoform 5).
/FTIG=VSP_006076.
Missing (in isoform 5).
/FTIG=VSP_006077.
S -> T (IN REF. 1).
S -> N (IN REF. 1).
S -> N (IN REF. 1).
S -> D (IN REF. 1).
S -> N (IN REF. 1).
                                        sterile alpha motif (SAM) domain SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing
                                                                                                                                                                                                                                          EMBL; AF102855; AAD04569.2; --
EMBL; AF131951; AAD29417.1; ALT_INIT.
EMBL; AF131951; AAD29417.1; ALT_INIT.
EMBL; AF141904; AAD2975.1; --
EMBL; AF141904; AAD2975.1; --
EMBL; AF141904; AAD2975.1; --
EMBL; AF141904; AAP02498.1; ALT_INIT.
INTERPO: IPR001478; PDZ.
INTERPO: IPR001478; PDZ.
INTERPO: IPR001478; PDZ.
INTERPO: IPR001452; SH3.
PFam; PF00536; SAM; I.
PFam; PF00536; SAM; I.
PFam; PF00518; SH3; I.
PFAMRT; SM00248; ANK; 6.
SMART; SM00248; ANK; 6.
SMART; SM00326; SH3; I.
PROSITE; PS5008; ANK_REPEAT; 3.
PROSITE; PS50006; SH3; I.
PROSITE; PS50106; PDZ; I.
PROSITE; PS50106; PDZ; I.
PROSITE; PS50106; SH3; I.
ANK 4.
REPEAT 212 245 ANK 4.
REPEAT 212 245 ANK 7.
DOMAIN 554 613 SAM.
DOMAIN 663 757 POLY-PRO.
DOMAIN 1010 1015 POLY-PRO.
DOMAIN 1850 1860 POLY-PRO.
DOMAIN 1850 1860 POLY-PRO.
PONAIN 1850 1860 POLY-PRO.
POLY-PRO.
POLY-PRO.
PANCE PROSITE: PROSITE PANCE PROSITE: PROSITE PAN
                       PDZ/DHR domain.
     ANK repeats
  SIMILARITY: Contains 7
SIMILARITY: Contains 1
SIMILARITY: Contains 1
SIMILARITY: Contains 1
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                                                                                                                     1608 LPAAPPPAVAAAPPTLDSTASSLTSYDSEVATLIQGAPAAPGDPPAPGPPAAPAPAP 1667
                                                                                                                                                                                                                                 ------DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTL 146
                                                                                                6 HIQNISNNKTERSTAPLNTQISALRNDP-----KPLPQQPPAPANQDQNSSQNTRLQ 57
                                                                                                                                                                58 PTPPIPAPAP------KPAAPP------RPLDRESPGVENKLIPSVGSPASS 97
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                  ---GLSQEQLEHRERS---LQTLRDIQRM--LFPDEKEFTGAQSGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-87089740; PubMed=2432395;

Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;

"Circumsporozoite protein of Plasmodium berghei: gene cloning and identification of the immunodominant epitopes.";

Mol. Cell. Biol. 6:3965-3972(1986).

-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIRCUMSPOROZOITE PROTEIN.

13 X 8 AA TANDEM REPEATS.

16 X 2 AA TANDEM REPEATS OF P-Q.

TSP TYPE-1.

E8068A6D11D9551B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 CSP_PLABE STANDARD; PRT; 339 AA. P06915; 01-JAN-1988 (Rel. 06, Created) 01-JAN-1988 (Rel. 06, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Circumsporozoite protein precursor (CS). Plasmodium berghei. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                              ; Score 146; DB 1; Length 2167;
; Pred. No. 0.96;
35; Mismatches 82; Indels 6
226333 MW; 3F478B5A7B18BA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLE.
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InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
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                              14.2%;
23.8%;
                      Query Match
Best Local Similarity 23.8%
Watches 56; Conservative
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ANCHORING THE
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1497 HVRFLEN-
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93
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339 2
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CSP_PLABE
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Search completed: October 15, 2003, 10:31:04 Job time: 25.4008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein

October 15, 2003, 10:27:33 ; Search time 112.475 Seconds (without alignments) 445.097 Willion cell updates/sec Run on:

US-09-915-543-15_COPY_199_392 1028 1 TIVSFHIQNISNNKTERSTA........LFPDEKEFTGAQSGGPQQNP 194 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 258052604 residues 830525 Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* p_human:* p_invertebrate:* sp_vertebrate:* SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rotus:*
12: sp_virus:*
13: sp_virus:*
15: sp_virus:*
16: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archeap:* o_mhc:* o_organelle:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	039620 chlamydomon 0994y9 neurospora 08w5k6 oryza sativ 091vnl arabidopsis 036027 schizosacch 099944 pneumocysti 057580 gallus gall 096951 homo sapien 09046 turkey herp 08dgul synechococc 099x57 deinococcus 039492 chlamydomon 09vzc2 drosophila 041805 zea mays (m P70433 mus musculu	
(1)	Q39620 Q9P4Y9 Q9P4Y9 Q9LVN1 Q36027 Q9P944 O57580 Q9P651 Q9DGT6 Q9DGT6 Q9DGT7 Q39492 Q9V2C2 Q41805 P70433	
DB	100 100 100 100 100 100 100 100	
å Query Match Length DB	473 473 1269 1307 1011 1151 1151 816 839 488 839 820 802 802	
% Query Match	12. 12. 12. 12. 12. 12. 12. 12. 12. 12.	
Score	177.5 167.5 167.5 162.5 162.5 161.5 160.5 160.5 160.5 158.5 158.5 158.5	
Result No.	1178460000011111111111111111111111111111111	

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Q9spm0 zea mays (m Q9xdh2 mycobacteri Q9fpq5 chlamydomon O65530 arabidopsis O22514 santalum al	Q9k117 mus musculu Q9kux2 arabidopsis Q9rf11 myxococcus Q9lj64 arabidopsis Q9akp3 rickettsia	Q26963 trypanosoma Q9h6k5 homo sapien Q81rm7 chlamydomon Q8vkn7 mycobacteri Q8vij6 mus musculu Q8uzb4 grapevine f Q9sbml volvox cart O15411 homo sapien	homo homo 6 mus caenc 13 arak 17 oryz 10 arak 15 arak
10 Q9SPM0 2 Q9XDH2 10 Q9FPQ5 10 Q6530 10 Q2514	110 77 77 77 77 77 77 77 77 77 77 77 77 77	5 11 10 10 10 10 10	4 Q96JK7 4 Q96L91 11 Q62106 5 Q9GZH1 10 Q9CS1 10 Q9CS1 10 Q9ZUE0 10 Q9ZUE0 10 Q9ZUE0 10 Q9ZUE0
.2 1315 .1 763 .0 386 .0 731 .9 326	.9 493 .8 883 .8 956 .7 602	7. 964 .7 1997 .6 598 .6 699 .6 309 .6 309	.6 1157 .6 3124 .5 188 .5 302 .5 712 .5 7201 .4 273 .4 752 .4 1202
156 15 155 15 54.5 15 54.5 15 53.5 14	153 14 152 14 152 14 152 14 152 14	51.5 151 151 151 151 14 50.5 14 150 14 150 14	150 149 149 149 149 148 148 148 148 148 148 148 148 148 148
118 118 119 119 11	⊣	28 23 33 33 33 33 33 33 33 33 33 33 33 33	36 33 33 33 33 34 44 44 55 44 11

ALIGNMENTS

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74 RPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN-NRAVTPVSQGSNSSSADPKA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                         STRAIN=CC-621;
MEDLINE=95093034; PubMed=8000007;
Woessner J.P., Molendijk A.J., van Egmond P., Klis F.M.,
Goodenough U.W., Haring M.A.;
"Domain conservation in several volvocalean cell wall proteins.";
Plant Mol. Biol. 26:947-960(1994).
EMBL; L29029; AAB53953.1; -.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                           Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBL_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 177.5; DB 10; Length 473; 30.5%; Pred. No. 1.7e-05; tive 19; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
38506131FAA674A4 CRC64;
                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                            473 AA
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473 P(
47532 MW;
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Best Local Similarity 30.54
Matches 46; Conservative
                                                                                              VSP-3 protein precursor. VSP-3.
                             PRELIMINARY;
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32 4
473 AA;
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NCBI_TaxID=3702;
  NCBI_TaxID=4530;
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  3 VSFHIQNISNNKT---ERS--TAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQ 57
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D Q8W5K6
PRELIMILL.
D Q8W5K6
AC Q8W5K6
DT Ol-MAR-2002 (TrEMBLrel. 20, Created)
DT Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT Ol-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DT Ol-WAR-2005 (TrEMBLrel. 23, Last annotation update)
DT Ol-WAR-2005 (TrEMBLrel. 23, Last sequence update)
DT Ol-WAR-2005 (TrEMBLrel. 20, Last sequence update)
OC SUNBA0079B05.10 OR OSJNAA0079B05.2.
OSJNBA0079B05.10 OR OSJNAA0079B05.2.
OC Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
C Spermatophyta; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                      09P4Y9;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
B11B22.30.
Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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100) to the EMBL/GenBank/DDBJ databases.
ABB92706.1; -.
165; P_rich_extensn.
195; RabGAP_TBC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 168.5; DB 3
; Pred. No. 0.00015;
24; Mismatches 61
                                                                                                                    SPSPAKKPSPPPVEEGAPPPI-EGPPPMEE 462
                                                                             PPPPVSSGEPPTLGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFKQLRLREEGSAPTGDDDEKSSTPEEKE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---QLEHRER-SLQTLRDIQRMLFPDEKE 181
                                                                                                                                                                                                                                                                                                                                                 PRT;
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Similarity 30.1%;
63; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. German Neurospora Submitted (MAY-200 EMBL; AL356834; CA
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  377
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Q8W5K6
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Q9P4Y9
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68 KPAAPPRPLDRESPGVENKLIPSVGSPA----SSTPLPPDGTGPNSTPNNRAVTPVSQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIP---APAP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC clones.";
DNA Res. 7:31-63(2000).
EMBL; AB019228; BAA96907.1; -.
InterPro; IPR003104; FH2.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF02181; FH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00498; FH2; 1.
SMART; SM00498; FH2; 1.
                                                                                                                                                                                                   Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R., Rambo T., Saski C., Henry D., Oates R., Simmons J.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC079179; AAL31655.1; -.

EMBL; AC116601; AAM08709.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%; Score 167.5; DB 10; Length 1269; 32.6%; Pred. No. 0.00025; live 9; Mismatches 61; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1307;
                          Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T., Saski C., Henry D., Oates R., Simmons J.; *Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138432 MW; 262E546481B25CA6 CRC64;
                                                                                                                    Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09LVN1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Gb|AAD23008.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GSNSSSADPKAPPPPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657 GIGNKFPAPPPPPPPRSSSRTPT 680
                                                                                                                                                                                                                                                                                                                                                                                        Gramene; Q8W5K6; -.
InterPro; IPR003104; FH2.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF02181; FH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00498; FH2; 1.
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nes 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 1269 AA;
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SEQUENCE FROM N.A.
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RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                            66 APKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNS 125
                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
                                                         9 NISNN -- KTERSTAPLNTQISALRNDPKP - LPQQPPAPANQDQNSSQNTRLQPTPPIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Gaps
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connor K., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST LAS17.
EMBL; AF038575; AAB92587.1; -.
EMBL; Z98980; CAB11718.1; -.
GeneDB_SPOMDE; SPAC4F10.15c; -.
               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 162.5; DB 3; Length 574; 30.9%; Pred. No. 0.00027; tive 21; Mismatches 64; Indels 27
              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     036027 PRELIMINARY; PRT; 574 AA.
036027;
036027;
01-JUN-1998 (TTEMBLIEL. 06, Created)
01-JUN-1998 (TTEMBLIEL. 23, Last sequence update)
01-JUN-1998 (TTEMBLIEL. 23, Last annotation update)
01-MAR-2003 (TTEMBLIEL. 23, Last annotation update)
Wiskott-aldrich syndrome protein homolog 1.
WSP1 OR SPAC4F10.15C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Zankel T.C., OW D.W.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO.
POLY-PRO.
L -> V (IN STRAIN JS21).
CGESEFCA6A02F0E4 CRC64;
                                                                                                                                                  126 SSADPKAPP------PPPVSSGEPPTLGE 148
                                                                                                                                                                 ; Pred. No. 0.00054;
18; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597; EVH1.
965; P_rich_extensn.
960; WH1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59605 MW;
   29.98;
               46; Conservative
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343
366
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GeneDB_SPombe; SPAC4F1(InterPro; IPR000697; EVINTERPRO; IPR002965; P_InterPro; IPR001960; WP Pfam; PF00568; WH1; 1, PRINTS; PR01217; PRICHE
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Best Local Similarity
Watches 50; Conserv
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SEQUENCE_FROM N.A.
Best Local Similarity
Matches 46; Conser
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SEQUENCE FROM N.P
STRAIN=JS21;
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DOMAIN
DOMAIN
VARIANT
SEQUENCE
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----PIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 23, Last annotation update)
High molecular mass nuclear antigen (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                               Pneumocystis carinii f. sp. muris.
Eukaryota, Fungi, Ascomycota, Pneumocystidomycetes; Pneumocystidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VIPVSQGSNSSSADPKAPPPPVSSGEP-----PTLGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780 PPKPTPQPTSEPAPQPTSESTSEP-TPRPPPQPTSEPTSEPTSEPTSEPSQPTPQ 834
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20184731; PubMed=10721706;
Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J.,
Weinberg G.A., Haidaris C.G.;
Weinberg G.A., Haidaris C.G.;
"Molecular characterization of KEX1, a kexin-like protease in mouse
Pneumocystis carinii.";
Gene 242:141-150(2000).
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
EMBL; AF093132; AAF32493.1; -..
MEROPS; S08.011; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98034404; PubMed=9365273;
Shimada K., Harata M., Mizuno S.;
"A nuclear matrix-associated high molecular mass nuclear antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%; Score 162.5; DB 3; Length 1011; 17.8%; Pred. No. 0.00046; Conservative 21; Mismatches 65; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1011 AA; 112021 MW; FBE472C8F65864E8 CRC64;
                                                 09P944;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kexin-like protease KEX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1151 AA
                         1011 AA
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InterPro; IPR000209; Peptidase_S8.
InterPro; IPR005970; PT.
InterPro; IPR002884; P_domain.
InterPro; IPR002965; P_rich_extensn.
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                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            Pneumocystis.
NCBI_TaxID=42066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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057580
Q9P944
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                                                                                                                                                                                       PKPLPQQPPAPANQDQNSSQNTRLQPTP-PIPAPAPKPAAPPRP-----LDRESPGVE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Muscle;

TISSUE=Muscle;

Strausberg R.;

Strausberg R.;

Strausberg R.;

Strausberg R.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

REMBL; BC009963; AAH07992.1; -.

REMBL; BC007404; AAH07992.1; -.

REMBL; BC007404; AAH30134.1; -.

REMBL; BC030134; AAH30134.1; -.

REMBL; BC030134; PAH30134.1; -.

REMBL; BC03021; MAP_kin.

REMBL; BC03021; MAP_kin.

REMBL; BC030290; Ser_thr_pkinase.
                                                                                                                                                39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Gaps
and marked decrease of its immunoreactivity during 's phase.":
                                                                                                                                                                                                                                                                                                                                                            096651 PRELIMINARY; PRT; 816 AA.
096651; 0969G1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mitogen-activated protein kinase 7.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ase; Serine/threonine-protein kinase; Transferase.
A; 88386 MW; 27729FE31658CE3B CRC64;
                                                                                                                       Query Match 15.8%; Score 162.5; DB 13; Length 1151; Best Local Similarity 33.1%; Pred. No. 0.00052; Matches 45; Conservative 12; Mismatches 40; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%; Score 161.5; DB 4; Length 816;
ty 32.1%; Pred. No. 0.00044;
ervative 7; Mismatches 64; Indels 43
                                                                                                2403F6835F9A2AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Pancreas, and Muscle;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; 1.
                                                 65; P_rich_extensn.
PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prot_kinase; 1.
              f S phase.";
3031-3041(1997).
24137.1; -.
                                                                                                109708 MW;
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                                                                                                                                                                                                                                                                        EPPTLGENPDGLSQEQ 157
                                                                                                                                                                                                                                                                                                  SPPDGPKAPSGAGEAE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; PRINTS; PR01217; PRICHE: Probom; PD000001; Prot. PROSITE; PS01351; MAPK;
                                                                                      1151
                                                                                     1151 115
1151 AA;
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             the progression of
J. Cell Sci. 110:3C
EMBL; D88440; BAA24
InterPro; IPR002965
PRINTS; PR01217; PF
NON_TER 1151
SEQUENCE 1151 AA;
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PROSITE; PS50011;
PROSITE; PS00108;
ATP-binding; Kinas
SEQUENCE 816 AA;
   chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Best Local S
Matches 54
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   HMNA, of
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Q96G51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NRASEROLA - DTAASALR - APSPVFWSAFDSRYPHLAPANOSNSDPLCPETSTASAOIL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 HINSPIPPISTSPAPIPSPIQPPACLPSPAPISSPVQPPALLPLIFSPIIPVEFIQPQSP 357
                                                                                                                    64 APAPKPAAPPRPLDRESPG-----VENKLIPSVGSPASSTP-----LPPPGT 105
                                                          577 RPAAPALTSVPAPAPAPTPTPTPVQPTSPPPGPVAQPTGPQPQSAGSTSGPVPQPACPPP 636
                                                                                                                                                                              637 GPAPHPTGPPGPIPVPAPPQIATSTSLLAAQSLVPPPGLPGSSTPGVLPYFPPGLPPPDA 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 NNKTERSTAPLNTQISALRNDPKPL-----PQQPP-APANQD-----QNSSQNTRL- 56
----QQPPAPANQDQNSSQNTRLQPTPPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tulman E.R., Afonso C.L., Lu 2., Zsak L., Rock D.L., Kutish G.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF243438; AAG14284.1; *.
EMBL; AF243438; AAG14273.1; *.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tulman E.R., Afonso C.L., In Z., Zsak L., Rock D.L., Kutish G.F.; "The genome of a very virulent Marek's disease virus."; J. Virol. 74:7980-7988(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
RS1 immediate-early gene transactivator ICP4-like protein (RS1
immediate-early gene transactivator-like protein),
MDV084 OR MDV100.
                                                                                                                                                                                                                                                                               106 G--PNS----TPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTLG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.6%; Score 160.5; DB 12; Length Best Local Similarity 32.4%; Pred. No. 0.0015; Matches 60; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005205; Herpes_ICP4_C.
InterPro; IPR005206; Herpes_ICP4_N.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03585; Herpes_ICP4_C; 1.
Pfam; PF03584; Herpes_ICP4_N; 1.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 2321 AA; 252959 WW; EF130EB0C4503003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses.
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MEDLINE=20392152; PubMed=10933706;
17 RSTAPLNTQISALRNDPKPLP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turkey herpesvirus.
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09DGT6
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Q9VZC2
           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                  -SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPP---PPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                                                                               PLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVG--
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LA., Heidelberg J.F., Hickey E.K., Peterson J.D., D.H., Gwinn M.L., Nelson W.C., Richardson D.L., H., Jiang L., Pamphile W., Crosby M., Shen M., Lam P., McDonald L., Utterback T., Zalewski C., Tavind L., Daly M.J., Minton K.W., Fleischmann R.D., Son K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                  Ś
                                                                                                                                                                   Sasamoto
                                                                                                                        SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermosphilic cyanobacterium Thermosynechococus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                 15.6%; Score 160; DB 16; Length 488;
larity 33.3%; Pred. No. 0.00035;
Conservative 17; Mismatches 51; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans.
Bacteria: Deinococcus-Thermus; Deinococcacea; Deinococcacea; Deinococcus.
NCBI_TaxID=1299;
QBDGU1;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serine/threonine protein kinase.
TLL2222.
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                 proteome.
. 52553 MW; 71287B898A6DBB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 839 AA; 79759 MW; 3B6C2CD0CFEFF4DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9RX57

O9RX57;

O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Hypothetical protein DR0458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 160; DB 16;
Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001904; AAF10038.1; -.
TIGR; DR0458; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10567266;
                                                                                                                                                                                                                                   DNA Res. 9:123-130(2002)

EMBL; AP005376; BAC09774.1; -.

Kinase; Complete proteome.

SEQUENCE 488 AA; 52553 MW;
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31.3%;
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.,
Dodson R.J., Haft J
Moffat K.S., Qin H
Vamathevan J.J., L.
Makarova K.S., Ara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Makarova K.S., Ara
Ketchum K.A., Nels
Fraser C.M.;
"Genome sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
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STRAIN=R1;
MEDLINE=20036896;
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Best Local
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Q9RX57
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Similarity

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                                                                    222 PIPNAPAQTPAPATQAPAAQTPTAQAPATQTPATPAPAAQRPAGGAPSPAPAQANAPA 281
                                                                                                                                                           282 GSVVPEATVPESSTPAAPSAQTPPTPTRETAQTEASPAAPNSSAAAPNEPASEPV-AGRP 340
                                               84
                                     33 PKP-LPQQPPAPANQDQNSSQNTRLQP---TPPIPAPA---PKPAAP-PRPLDRESPGVE
                                                                                                                      85 NKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGS-NSSSADPKAPPPPVSSGEP
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         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=UTEX 10;
MEDLINE=95093034; PubMed=8000007;
Woessner J.P., Molendijk A.J., van Egmond P., Klis F.M.,
Goodenough U.W., Haring M.A.;
"Domain conservation in several volvocalean cell wall proteins.";
Plant Mol. Biol. 26:947-960(1994).
EMBL; L29028; AAB53954.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas eugametos.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG15021 protein (RE17165p).
CG15021.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                      144 PTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGG 189
                                                                                                                                                                                                                                                       ----PDTAASAGTPSAG 374
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      Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.4%; Score 158.5; DB 10; Best Local Similarity 30.9%; Pred. No. 0.00032; Matches 46; Conservative 15; Mismatches 71;
   79;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VSQGSNSSSADPKAPP--PPPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                              351
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                                                                                                                                                                                                                                             341 GTAASSPESASPVTVTPRGET----
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 13;
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351 PC
35310 MW;
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01,
23,
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01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2003 (TrEMBLrel. 2
WP6 protein precursor.
Conservative
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3053;
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                                                        RC STRAIN—Berkeley;

RX MEDLINE—20196005; PubMed=10731132;

RR Adams M.D. Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
Adams M.D. Lewis S.E., Richards S., Ashburner M., Hedderson S.N.,
RA Sutton G.G., Wortnam J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burli J.F., Agbayani A., Am H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktarolu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktarolu L., Beasley E.M.,
Besson K.Y. Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Putller H., Cadieu E., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Lauller C., Davenport L.B., Davies P.M.,
A cepalos B., Delcher A., Deng Z., Mays A.D., Davies P.M.,
Burtis K.C., Gabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Codor K., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Harris N.L., Hustov P.D., Heiman T.J., Hernandez J.R., Harris M.,
Alli M., Kalush F., Karpen G.H., Kez Y. Kenningson J.M., Ketchum K.A.,
Alli M., Kalush F., Karpen G.H., Kez Y. Kenningson J.M., Mattor B., McIntosh T.C., Morris J., Wel M.-H., Iloeywan C.,
Allali M., Kalush F., Karpen G.H., Kez Y. Kenningson J.M., Mattor B., McIntosh T.C., Morris J., Wel M.-H., Indey W. Lin X.,
Alli M., Woodage T., Simpson M., Strong R., Shon H.,
Rahe B.C., Siden-Kiamos I., Simpson M., Strong R., Shon H.,
Rahe B.C., Siden-Kiamos I., Simpson M., Strong R., Shon H.,
Ray Leng X.H., Woodage T., Worley G., Mullans S.M., Woodage T., Simpson M., Strong R., Shon H.,
Ray Leng X.H., Woodage T., Shon M., Zhong G., Zhan K., Zhan M., Zhong G., Zhan M., Zhong G., Zhan K., Shon H.,
Ray Leng K.H., Perker B.W., Rubin G.M., Weissebach J.,
Ray Leng K.H., Myers B.W., Rubin G.M., Weissebach T.,
Ray Leng R.H., Perker B.W., Rubin G.M., Weissebach M.,
Ray Leng R.H., Myers B.W., Rubin G.M., Weissebach M.,
Ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Frise E., Galle R.F., Garg N.S., George R.A.,
W., Frise E., Galle R.F., Mattei B., Moshrefi A.,
Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Paragas V., Park S., Patel S., Pfeiffer B.,
Ong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
M., Strong R., Svirskas R., Tector C., Tyler D.,
M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
G of Drosophila melanogaster genome.";
(MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Guang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
  rosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nce of Dro
2195(2000)
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Dodson K., Dorsett
Ferriera S., Frise
Gonzalez M., Houck
Ibegwam C., Jalali
McIntosh T.C., Moy
Pacleb J., Paragas
Phouanenavong S., P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence Science 287:2185-27 [2]
SEQUENCE FROM N.A. Celniker S.E., Adam
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Banzon J., An H.,
Carlson J.W., Cent
                                                   z
 Ephydroidea; Dra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Misra S.,
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91 VG-----SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 YGPPQTPPPRPPPQPTPSAPAPPSYGPPQTPPPRPPPQPTPSAPAPSYGPPQPPAPQ
                                                                                                                                                                                                                      STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=B73; TISSUE-Pollen;
Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.;
"Pex genes: pollen-specific genes with extensin-like domains.";
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; Z34465; CAA84230.1;
InterPro; IPR001611; LRR.
InterPro; IPR002965; P_rich_extensn.
                                 C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 158.5; DB 5; Length 420; 29.6%; Pred. No. 0.00038; ive 11; Mismatches 64; Indels 25
                       S.E., Gibbs R.A., Rubin G.M., Venter to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003481; AAE47902.2; -.
EMBL; AY071124; AAL48746.1; -.
FLYBase; FBGN0035544; CG15021.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
SEQUENCE 420 AA; 42947 MW; 96D62FFDC9F996E1 CRC64;
                                                                                                                                               Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2C77C7F8D7130149 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Extensin-like protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1188 AA
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PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                     Adams M.D., Celniker
Submitted (MAR-2000)
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1188 AA;
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                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A
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Best Local
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SIGNAL
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3;

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RAY MCBL_IGALID-10030;

RAY MCBL_IGALID-10030;

RY SEQUENCE FROW N.A., AND CHARACTERIZATION.

RY TISSUE-BRAIN.

REDIINE-97015079; PubMed-8861907;

REDIINE-97015079; PubMed-8861907;

RY Mond, a relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";

RY MOND, a relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";

RY MOND, A relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";

RY MONTILITY. INDUCES THE FORMATION OF F-ACTIN RICH OUTGROWTHS IN FUNCTION: LOCALIED TO FOCAL ADHESIONS AND, TO A LESSER EXTENT, LEADING EDGES AND STRESS FIBERS.

-1 - RIEBRAITYPE PRODUCTS: 4 ISOFORMS; MENA, MENA+, MENA++ AND MENA+++ (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1 - RIEBRAITYPE PRODUCED BY ALTERNATIVE SPLICING.

-1 - ALTERNATIVE ACC5266-1; - .

BR MEL; U7252; AAC5266-1; - .

BR MEL; U7252; AAC5266-1; - .

BR MED; U7252; AAC5266-1; - .

BR MED; U7252; AAC5266-1; - .

BR MIL: 107521; AAC5666-1; - .

BR MIL: 107522; AAC5866-1; - .

BR MOD: MIL: 108360; Enabl).

BR MOD: MIL: 10840 MIL: 1087 MIL: 1087 MIL: 1087 MIL: 10840 MIL: 1087 MIL: 10840 MIL: 10840 MIL: 1087 MIL: 1087
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                                                                                                                                                                       P-----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP---PDGTGPNSTPNNRAVTPV 119
                                                                                       -- TPPIPAPAPK
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POLY-PRO.
POLY-PRO.
POLY-PRO.
POLY-PRO.
POLY-RG.
POLY-RG.
PHOSPHORYLATION (BY CAPK AND CGPK) (BY SIMILARITY).
PHOSPHORYLATION (BY CAPK AND CGPK) (BY SIMILARITY).
MISSING (IN ISOFORM MENA++).
MISSING (IN ISOFORM MENA AND ISOFORM MENA+).
CIFC -> VFYL (IN ISOFORM MENA++).
MISSING (IN ISOFORM MENA++).
MISSING (IN ISOFORM MENA++).
MISSING (IN ISOFORM MENA+).
                                             19; Gaps
                                                                                                                                                                                                                                                                                                                                                           RESULT 15
P70433
ID P70433 PRELIMINARY; PRT; 802 AA.
AC P70433; P70431; P70432;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FBB-1997 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENABLED homolog.
GN ENAH OR MENA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
      Length 1188;
                                             Indels
                                                                                  KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP
 15.4%; Score 158.5; DB 10; 32.0%; Pred. No. 0.0011; ive 17; Mismatches 68;
                                                                                                                                                                                                                                                                                      PPAPVSSPPPPVKSPPPPAPVSSPPPPIKSPPP 1110
                                                                                                                                                                                                                                                             SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
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Query Match
Best Local Similarity 32.03
Matches 49; Conservative
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348 NKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS 407
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                                                                                                                 34 KPLPQQPPAPANQDQN------SSQNTRLQPTPPIPAPAPKPAAPPRPL---
                                  88;
      Length 802;
                                                                                                                                                                                                                               ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                           528 QPAESPIPQG--LVLGPPAPPPPPPLPSGPAYASALPPPPGPPP 569
                                  Indels
   15.4%; Score 158; DB 11; 26.3%; Pred. No. 0.00079; ive 15; Mismatches 62;
                                                              --QISALRNDP-
Query Match
Best Local Similarity 26.3
Matches 59; Conservative
                                                          13 NKTERSTAPLNT--
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Search completed: October 15, 2003, 10:35:50 Job time: 115.475 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 15, 2003, 10:27:32 Run on:

; Search time 21.5175 Seconds (without alignments) 258.182 Million cell updates/sec

US-09-915-543-15_COPY_349_383 178 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

A_Geneseq_19Jun03:*

1: SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
3: SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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6: SIDS1/gcgdata/geneseqp-embl/AA1985.DAT:*
7: SIDS1/gcgdata/geneseqp-embl/AA1986.DAT:*
8: SIDS1/gcgdata/geneseqp-embl/AA1989.DAT:*
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11: SIDS1/gcgdata/geneseqpenembl/AA1991.DAT:*
13: SIDS1/gcgdata/geneseqpenembl/AA1993.DAT:*
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19: SIDS1/gcgdata/geneseqpenembl/AA1993.DAT:*
10: SIDS1/gcgdata/geneseqpenembl/AA1993.DAT:* SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

number of results predicted by chance to have a or equal to the score of the result being printed, analysis of the total score distribution. number of C, Pred. No. is the score greater that and is derived by

SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:* /gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:

			Description		Human legless homo	Holomod P.T.S nemily	POTOMOTI CAPOR CONCOR	monse pera-carentu	Mouse beta-catenin	Human hota-catorin	יותיימיו הבית כמרביודוו	Human legless homo	Drosophila melanog	FORTER THE STATE OF THE STATE O	D. melanodaster id	Asperdillus fumida	,
COLUCTION			ID		AAB71229	ABB11808	AA1178461	1010	AAU78460	AAI178463	0000000	MAB / 1230	ABB58779	000014044	PAD/1220	ABJ25853	
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			Match Length DB ID	1 ((• • • • • • • • • • • • • • • • •	14.2b	1435	320	1	1494	738		CTTT	1429	1464	**	603	
	ф	Query	Match	1000	0.001	100.0	61.2		61.2	60.1		7.00	37.1	1 22	1	32.3	
			Score		۵/۲	178	109	1 4	TOA	107	101	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	99	7	2	57.5	
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ABJ26453	0 0	200	20 0	300	AAG63852	AAB68522	AAB92828	ABG96281	ABG96282	528	æ		7	4	4	AAB86347	S	ABP43969	AAG13171	AAU33491	ABP47770	AAU35058	AAG89346	н	AAY41139	ABB69662	96	05	S	76	55	AAB07850	S	436	AAY42781
24	1 6	770	7 (77	22	22	22	23	23	23	23	22	22	22	22	22	21	23	21	22	23	22	22	22	20	22	23	21	21	55	21	21	22	21	50
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ALIGNMENTS

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Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                   Human legless homologue lgs/bc19 protein,
                      AAB71229 standard; Protein; 1426 AA
                                                                                                                                                                                                                                27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                      28-JUL-2000; 2000US-221502P
                                                                (first entry)
                                                                                                                                                                                                                                                                          (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
(KRAM/) KRAMPS T.
(PETE/) PETER O.
                                                                                                                                                                                     US2002086986-A1
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                           04-JUL-2002.
                                                               18-NOV-2002
                                           AAB71229;
RESULT 1
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Peter 0;

Kramps T,

Froesch B,

Brunner E,

Basler K,

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factor;
                                                                                                                                                            This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue 1gs/bc19 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                     useful in therapeutic method for treating disorders as cell differentiation or cell proliferation .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 178; DB 23; Best Local Similarity 100.0%; Pred. No. 8.6e-16; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BCL9 homologue, SEQ ID NO:2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 1435 AA
                                                                                                                            English.
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                                                                                                                                                                                                                                                                                                                                                                          invention.
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27-APR-2000; 2000US-0560875
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                                                                                                                            B; 41pp;
                      68
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                                                                                                                                                                                                                                                                                                                                                      human legless (lg:
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                                                                      Novel polypeptide of cell fate such
                    2002-635689/
                                     N-PSDB; AAF88467
                                                                                                                        Example II; Fig
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ABB11808
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and conserved ABB10981-ABB12330 represent nucleic acids encoding them. The convention also relates to vectors and recombinant host cells comprising a unreaction also relates to vectors and recombinant host cells comprising a uncleotide of the invention, methods of producing the novel polypeptides, methods of detecting the nucleotides or the invention. Methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which propertides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to propertides of the invention may differential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention activities; stem cell growth factor activity; differential therapeutic activities; promodulatory activities; promodulatory activities; promodulatory activities, and mencential therapy activities or involved in oncogenesis. Cancer or language of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders or expected or lymphoid cell proliferation are useful for preventing, treating or ameliorating medical cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell proliferative retinopathy atheroscierosis, coronary heart disease.

Conditions, e.g., by protein or gene therapy. Such conditions or replant or proliferative retinopathy atheroscierosis, organization and repair growth. Polypeptides involved with tissue regeneration and repair growth. Polypeptides involved with tissue regeneration and repair growth. Polypeptides involved with the repeated or such dingal infections in addition to immune di
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                                                         Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 178; DB 22; ilarity 100.0%; Pred. No. 8.7e-16; Conservative 0; Mismatches 0;
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                                                                                                                                            Claim 20; Page 256-257; 1963pp; English.
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                                                                                                      e.g. arthritis and cancer
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WPI; 2001-457740/49
N-PSDB; ABA09052.
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Matches 35; Conserv
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Drmanac RT

Liu C,

Tang YT, (HYSE-)

HYSEQ INC

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Claim 1; Page 81-88; 113pp; Japanese
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N-PSDB; ABK47638.
                                                                          1494 AA;
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ses 21; Conserv
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                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                        of
                                                                                                                                                                            and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence c mouse beta-catenin nuclear localised protein #2.
                                                                                                                     New beta-catenin nuclear localised protein for diagnosis and trea of diseases associated with nuclear localisation of beta-catenin
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                                                                                                                                                                     ates to a beta-catenin nuclear localised
                                                                                                                                                                                                                                                                                                                                                                                                   protein; cancer;
tag.
                                                                                                                                                                                                                                            Score 109; DB 23;
Pred. No. 6.3e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  nuclear localised protein
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                                                                                                                                                     92; 113pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                    Protein; 1494
                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                           61.2%;
84.0%;
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                                               22-SEP-2000; 2000JP-0287876.
                               19-SEP-2001; 2001WO-JP08140
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                                                                                               36,
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N-PSDB; ABK47631.
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Best Local Similarity
Matches 21; Conser
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                                                                                               WPI; 2002-330014/
                                                                                                       N-PSDB; ABK47632.
                                                                                                                                                     Claim 2; Page 91-
                                                                                                                                                                     The invention rel
                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; EST
WO200224738-A1
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                28-MAR-2002
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AAU78460
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of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                     Gaps
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The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence c mouse beta-catenin nuclear localised protein.
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Pred. No. 3.5e-06;
1; Mismatches 0;
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Pred. No. 3e-06;
3; Mismatches
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ilarity 84.0%;
Conservative
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Best Local Similarity 87.5%;
Matches 21; Conservative
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(first entry)

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26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue higs-1 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                useful in therapeutic method for treating disorders as cell differentiation or cell proliferation -
                                                                                                                       Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
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Pred. No. 4.8e-06;
3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                             Peter 0;
                                                                                                  Human legless homologue hlgs-1 partial protein.
                                                                                                                                                                                                                                                                                                                                                             Kramps T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 GLSKEQLEHRERSLQTLRDIERLL 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 1429 AA
                                  Protein; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10B; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                             Froesch B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.1%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                               US-0915543
                                                                                                                                                                                                                                                                      28-JUL-2000; 2000US-221502P
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                             Basler K, Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-635689/68.
N-PSDB; AAF88468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB58779 standard;
                                                                                                                                                                                                                                                                                          (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
                                                                                                                                                                                                                                                                                                                           KRAMPS T.
PETER O.
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide of cell fate such
                                 AAB71230 standard
                                                                                                                                                                                                                                                27-JUL-2001; 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1115
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                                                                                                                                                                                                    US2002086986-A1
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                           04-JUL-2002.
                                                                             18-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB58779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                       AAB71230;
                                                                                                                                                                                                                                                                                                                            (KRAM/)
(PETE/)
          AAB71230
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3129; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.1%; Score 66; DB 22; Length 1429; 31.4%; Pred. No. 3.1; tive 10; Mismatches 14; Indels
Drosophila melanogaster polypeptide SEG ID NO 3129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: :| :||| | :: : : |||: : ||| | 520 ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB71228 standard; Protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D. melanogaster lgs protein.
                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                   Drosophila melanogaster.
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es 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL02882
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                                                                                                                                                                                        WO200171042-A2.
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                                                    Drosophila; de
pharmaceutical
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                                                                                                                                                                                                                                                                                                         This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the Drosophila melanogaster (fruitfly) legless (1gs) protein described in
                                                                                                                                                                                                                                      useful in therapeutic method for treating disorders as cell differentiation or cell proliferation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus essential gene protein #511.
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ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA 549
                                                                                                                                                                      Kramps T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
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                                                                                                                                                                      Froesch B,
                                                                                                                                                                                                                                                                                 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-285697P.
2001US-287066P.
2001US-295890P.
2001US-303899P.
2001US-316362P.
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                             27-JUL-2001; 2001US-0915543.
                                                     28-JUL-2000; 2000US-221502P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ervative
                                                                                                                                                                      Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus.
                                                                                                                                                                                               .68
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Best Local Similarity
Matches 11; Conserv
                                                                                               BRUNNER E.
FROESCH B.
KRAMPS T.
                                                                                                                                                                                                                                          Novel polypeptide of cell fate such
                                                                                    BASLER K.
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                                                                                                                                                                                               WPI; 2002-635689,
                                                                                                                                                                                                              N-PSDB; AAF88466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the disclosure or
                                                                                                                                         (PETE/) PETER O.
                                                                                                                                                                                                                                                                                    Example II; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200286090-A2
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27-APR-2001;
05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2002;
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 04-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                 (BASL/)
(BRUN/)
(FROE/)
(KRAM/)
                                                                                                                                                                     Basler
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify and sequences of other related or distant pathogenic organisms to identify and of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention.
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                                                                                                                                                                                                                New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                            Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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                                                                         Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus fumigatus essential gene protein #1111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24;
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                                                                         Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page -; 175pp; English.
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                                                                   Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-2002; 2002WO-US13142.
(ELIT-) ELITRA PHARM INC.
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                                                                   Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                  WPI; 2003-093124/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603 AA;
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                                                                         Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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the invention instance to mover purinted or isolated nucleic acids of the invention issued to treat a non-infections by a pathogenic to the invention are used to treat or prevent infections by a pathogenic corpanism such as A. fumigatus, to treat a non-infections disease in a subject (e.g. cancer), to prevent or contain contamination of an object biofilm comprising A. fumigatus. The polymucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of the protein invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                      New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel purified or isolated nucleic acids of
                                                                                                                                                            Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                            Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 17298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.3%; Score 57.5; D
Best Local Similarity 31.4%; Pred. No. 19;
Matches 11; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 1294 AA.
                                                                                                                                                                                                                                                                                                                                       -; 175pp; English.
                                                                                                                                                            Zamudio C,
 1US-285697P.
1US-287066P.
1US-295890P.
1US-303899P.
23-APR-2001; 2001US-285697P.
27-APR-2001; 2001US-287066P.
05-JUN-2001; 2001US-295890P.
09-JUL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      st entry)
                                                                                                                   (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                          Tishkoff D,
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                                                                                                                                                                                                  WPI; 2003-093124/
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page
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                                                                                                                                                                                                                                                                                                   e.g. cancer
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ID ABB63502
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                                                                                                                                                            B
                                                                                                                                                          Jiang
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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto J;
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                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 17298; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 1294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%; Score 56; DB 45.5%; Pred. No. 68; tive 6; Mismatches
                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:16943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 LQQQQAESQEQQASTLRDLERL 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95073 standard; Protein; 294 AA
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                                                                                                                                             Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126.
                                       23-MAR-2001; 2001WO-US09231.
                                                                   23-MAR-2000; 2000US-191637P,
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.5
Matches 10; Conservative
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                                                                                                                                            Adams M,
                                                                                                                                                                       WPI; 2001-656860/75
                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 AA;
                                                                                                                                                                                     N-PSDB; ABL07605
                                                                                                                                                                                                                                                interactions -
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            27-SEP-2001.
                                                                                                                                        Venter JC,
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence.

Complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 3'-end sequence complementary to a
polynucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
configurally full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13629 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Otsuki T;
                                                                                                                                                                               Claim 8; SEQ ID 16943; 2537pp + CD ROM; English.
 Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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GLRTEGLFRRSASVQTVREIQRL 246
 Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GLSQEQLEHRERSLQTLRDIQRM 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG96285 standard; Protein; 390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%;
52.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.22,
Lac 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention.
 Sugiyama T,
                                    WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 AA;
                                                                                                                        and/or diagnosis
full-length cDNAs
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Ishii S,
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ABG96285
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial or viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatcus orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disorders (e.g. inchiberculous granulomatcus orchitis), determining whether ovarian cancer has metastasized or is likely to metastasizing the ovarian cancer has metastasized or is likely to metastasizing the ovarian cancer nat risk of developing ovarian cancer. The present mains action represents one of the ovarian cancer markers
                                                                                                                                                                                                                                                                                               Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient -
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                                                                                                                                                                Kovatis SG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                          Hoersch S, Kamatkar S, Kov
andt PJ, Sen A, Vieby PO,
, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 134-135; 481pp; English.
                                                                                                                                                                                 Morrisey MP, Olandt PJ, S
Lu K, Schmandt RE, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GLRTEGLFRRSASVQTVREIQRL 203
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10-AUG-2001; 2001US-311732P.
19-SEP-2001; 2001US-323580P.
26-SEP-2001; 2001US-324967P.
26-SEP-2001; 2001US-325102P.
26-SEP-2001; 2001US-325149P.
                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   described in the invention.
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                                                                                                                                                                Gannavarapu M,
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                                                                                                                                                                                                                                         2002-723277/78.
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                                                                                                                                                                                                                                                            N-PSDB; ABS76377
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Local S. ...
12;
                                                                                                                                                                Monahan JE,
                                                                                                                                                                                  Meyers RE,
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Domain
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    Domain
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'note= "potential protein kinase phosphorylation site for casein kinase II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "potential protein kinase phosphorylation
site for tyrosine kinase"
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                                                                                                                                                                                                                                                       note= "potential protein kinase phosphorylation
    site for casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "potential protein kinase phosphorylation
    site for protein kinase C"
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    site for casein kinase II"
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                                                                         "potential protein kinase phosphorylation
site for tyrosine kinase"
                                                                                                                                    note= "potential protein kinase phosphorylation
    site for tyrosine kinase"
                                                                                                                                                                                               note= "potential protein kinase phosphorylation
    site for protein kinase C"
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/note= "GTPase-activator domain"
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110..350
'not.e= "GTPase-activator domain"
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                            Location/Qualifiers
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Homo sapiens
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/57. WPI; 2001-522598, N-PSDB; AAH74978 A substantially purified GTPase activating protein useful for treating or preventing cell signalling, immune and cell proliferative disorders including cancer especially colon cancer or preventing cel including cancer

E; 78pp; English. Claim 14; Fig 1A

The present sequence represents a human GTPase activating protein, designated GTPAPI. GTPAP polynucleotides and polypeptides are useful for treating or preventing a disease or condition associated with altered expression of GTPase activating proteins, especially cell signalling, immune and cell proliferative disorders, including cancer especially colon cancer. Examples of diseases treatable include

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sclerosis.
arteriosclerosis, diabetes, psoriasis, hepatitis and multiple scleros. GTPAP1 polynucleotides are also useful for gene therapy treatments of the diseases.
                                                                                                         Gaps
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/note= "potential protein kinase phosphorylation
site for casein kinase II"
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    site for tyrosine kinase"
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    site for tyrosine kinase"
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    site for casein kinase II"
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    site for protein kinase C"
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                                                                               22; Length 433;
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                                                                              DB
28;
                                                                                                      4; Mismatches
                                                                             Score 55;
Pred. No.
                                                                                                                                              224 GLRTEGLFRRSASVQTVREIQRL 246
                                                                                                                               2 GLSQEQLEHRERSLQTLRDIQRM 24
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                        AAG63852 standard; Protein; 433 AA.
                                                                             30.9%;
52.2%;
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                                                                       Query Match
Best Local Similarity 52.29
Matches 12; Conservative
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WO200161010-A2.

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                                                                                                                                                                                                                                                A substantially purified GTPase activating protein useful for treating or preventing cell signalling, immune and cell proliferative disorders, including cancer especially colon cancer -
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                                                                                                                                                                       Stewart EA,
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N-PSDB; AAH74979.
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                                                                                                                                                                                                                                                                                                                Claim 14; Fig 2A-
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                                             23-AUG-2001.
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Search completed: October 15, 2003, 10:30:24 Job time: 23.5175 secs

224 GLRTEGLFRRSASVQTVREIQRL 246

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein October 15, 2003, 10:27:32; Search time 7.08171 Seconds (without alignments) 209.113 Million cell updates/sec Run on:

US-09-915-543-15_COPY_349_383 178 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

seqs, 42310858 residues 328717 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued_patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 32, Appl				equence 15, Appl					Sequence 54, Appl							14,	14,	Sequence 11, Appl	Sequence 11, Appl	522(2257	227		31361,	315	equence 3, Appli
	Des	Sec	Se	Se	Se	Se	Se	Se	Se	Se	Se	Se	Se	Šě	Se	Š	Se	Se	Se	Se	Se	Se	Se	Se	Se	Se	Se	Se
	ID	US-09-507-765-32	-507-7	S-09-507-7	-252-9	-651-6	3-05	-09-252-5	Ϋ́	-09-252-6	-247-	-542-7	-252-9	19-186-276B-5	842-445-5	-186-188B-5	-252-9	-188-5	-715		8-646-715-1	-09-107-532A-5	US-09-252-991A-22579	2274	-252-991A-292	-252-991A-313	-09-134-001C-31	US-08-227-536-3
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us-09-507-765-30

Sequence 30, Application US/09507765; Patent No. 6509155; Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: Klinger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
FILE REFERENCE: PC-0010 US
CURRENT APPLICATION NUMBER: US/09/507,765
CURRENT FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGRAM
SEQ ID NO 30
LENGTH: 433

Sequence 3, Appli Sequence 5104, Ap Sequence 3753, Ap		Sequence 23336, A Sequence 6561, Ap Sequence 16908, A	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli	चे चे ले	Sequence 4, Appli Sequence 395, App Sequence 19252, A	Sequence 34, Appl
PCT-US95-04682-3 US-09-107-532A-5104 US-09-107-532A-3753	US-09-252-991A-18906 US-09-252-991A-31012	US-09-252-991A-23336 US-09-328-352-6561 US-09-252-991A-16908	US-08-466-390-4 US-08-470-950-4 US-08-467-781-4	US-08-195-487-4 US-08-483-924-4 US-09-452-294-1	PCT-US93-06160-4 US-08-858-207A-395 US-09-252-991A-19252	US-08-690-011A-34
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26.1 26.1 26.1	25.8 25.8	25.8 25.8 .8	25.8 25.8 25.8	25.8 25.8 25.8	25.8 25.6 25.6	25.3
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ALIGNMENTS

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Gaps
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US-09-507-765-32
                            Sequence 32, Application US/09507765;
Patent No. 6509155;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Klinger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Yue, Henry
TILLE OF INVENTION: GTPASE ACTIVATING PROTEINS;
FILE REFERENCE: PC-0010 US
CURRENT APPLICATION NUMBER: US/09/507,765
CURRENT FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 32
LENGTH: 333
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Best Local Similarity 52.2°
Matches 12; Conservative
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RESULT 1
US-09-507-765-32
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RESULT 5
US-09-651-656-15
Sequence 15, Application US/09651656
Fatent No. 6340566
GENERAL INFORMATION:
APPLICANT: MCCUTHEN MALONEY, SANDRA
TITLE OF INVENTION:
DIA DAMAGE AND DIA MISMATCHES
TITLE OF INVENTION:
TITLE OF INVENTION:
DIA DAMAGE AND DIA MISMATCHES
TITLE OF INVENTION:
TITLE OF INVENTION:
DIA DAMAGE AND DIA MISMATCHES
CURRENT RAPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 819
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Sequence 15, Application US/09650855
Sequence 15, Application US/09650855
Sequence 15, Application US/09650855
GENERAL INFORMATION:
APPLICANT: MACUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MISMATCHES
TITLE OF INVENTION: MISMATCHES
TITLE OF INVENTION: MISMATCHES
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN Ver. 2.1
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            6; Indels
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         9; Mismatches
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        13; Conservative
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SEQ ID NO 15
LENGTH: 819
TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25843
LENGTH: 1242
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                                                                                                                                              30.9%; Score 55; DB 4; Length 433; 52.2%; Pred. No. 9.1; 7; Indels tive
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                                                                                  Incyte ID No. 6509155 3068538CD1
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GTPASE ACTIVATING PROTEINS
0010 US
I NUMBER: US/09/507,765
:: 2000-02-18
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Elizabeth A.
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35.1%;
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Best Local Similarity 52.2%
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                              lens
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LENGTH: 433
                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
TYPE: PRT
ORGANISM: Homo sapi
                                                        ; NAME/KEY: misc_feat; OTHER INFORMATION: US-09-507-765-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feat
CTHER INFORMATION:
US-09-507-765-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sap
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US-09-252-991A-25843
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Wed Oct 15 11:

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; TYPE: PRT
; ORGANISM: SOYBEAN
US-09-247-373B-54
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US-09-542-749A-2
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
07196.136
N NUMBER: US/09/252,991A
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: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
07196.136
                                                                                 J. Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

NI: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

107196.136
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US-09-252-991A-24834

Sequence 24834, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

ITLE OF INVENTION: NUCLEIC ACID AND AMINO A.

ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24834

LENGTH: 589
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Sequence 23906, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS;
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23906
LENGTH: 578
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APPLICANT: Marc J. Rubenfield et al.; TITLE OF INVENTION: NUCLEIC ACID AND AMIN; TITLE OF INVENTION: AERUGINOSA FOR DIAGNO; FILE REFERENCE: 107196.136; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                 NUMBER: US/09/252,991A
: 1999-02-18
UMBER: US 60/074,788
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NUMBER: US 60/074,788
: 1998-02-18
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US-09-252-991A-23906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.2%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: O'KEEFF, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 54
LENGTH: 221
                                                                                                                                                                                                                    Length 354;
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GENERAL INFORMATION:

APPLICANT: Joergensen, Steen T.

APPLICANT: Christensen, Christina L.

APPLICANT: Christensen, Tina

TITLE OF INVENTION: A Bacillus Protein Production Cell

FILE REFERENCE: 5861.200-US

CURRENT APPLICATION NUMBER: US/09/542,749A

CURRENT FILING DATE: 2000-04-04

PRIOR FILING DATE: 1999-04-20

PRIOR FILING DATE: 1999-04-16

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 6

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 275

LENGTH: 275
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                                                                                                                                                                                                                                                                                                                                      2 GLSQE----QLEHRERSLQTLRDIQRMLFPDEKE 31
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Pred. No. 21;
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PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 28779 LENGTH: 354
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; Patent No. 6168954
; GENERAL INFORMATION:
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; Patent No. 6428981
                                                                                                                 TYPE: PRT; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28779
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Best Local Similarity 36.7
Matches 11; Conservative
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Length 275;

DB 4;

Score 50;

28.1%;

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                                                                                                                                              Sequence 56, Application US/08842445A

Sequence 56, Application US/08842445A

Patent No. 6441270

GENERAL INFORMATION:

TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses:
TITLE OF INVENTION: Thereof

FILE REFERENCE: 5914-056-999

CURRENT APPLICATION NUMBER: US/08/842,445A

CURRENT FILING DATE: 1997-04-24

EARLIER APPLICATION NUMBER: 08/638,617

EARLIER FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 79

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56

LENGTH: 524
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Sequence 56, Application US/09186188B

Patent No. 6455672

GENERAL INFORMATION:

APPLICANT: Benfey et al.

IITLE OF INVENTION: Thereof

FILE REFERENCE: 5914-074-999

CURRENT APPLICATION NUMBER: US/09/186,188B

CURRENT FILING DATE: 1999-11-05

PRIOR FILING DATE: 1997-04-24

PRIOR FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 79

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 73;
8; Mismatches 1
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                      5 QEQLEHRERSLQTLRDIQRMLFPDEKEFTG
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; ORGANISM: Plant
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(524)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-186-188B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.5%;
30.0%;
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Best Local Similarity 30.0%
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; ORGANISM: Plant
US-08-842-445-56
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US-09-186-188B-56
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LENGTH: 524
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ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
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US-09-186-276B-56
Sequence 56, Application US/09186276B
Sequence 56, Application:
Sequence 56, Application
Sequence 56, Application NUMBER: US/09/186,276B
CURRENT APPLICATION NUMBER: US/09/186,276B
SETIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1997-04-24
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.3e+02;
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                      10; Indels
                                                                                                                     RESULT 12
US-09-252-991A-32259
iSequence 32259, Application US/09252991A
iPatent No. 6551795
iGENERAL INFORMATION:
iTITLE OF INVENTION:
iTITLE OF INVENTION:
iTITLE OF INVENTION:
CURRENT APPLICATION NUCLEIC ACID AND AMINO A
iTITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIFILE REFERENCE: 107196.136
iCURRENT APPLICATION NUMBER: US/09/252,991A
iCURRENT FILING DATE: 1999-02-18
iPRIOR FILING DATE: 1998-02-18
iPRIOR FILING DATE: 1998-07-27
iNUMBER OF SEQ ID NOS: 33142
iSEO ID NO 32259
iLENGTH: 1201
iTYPE: ppm
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39.1%; Pred. No. 1...
 37.0%; Pred. No. 26; ive 7; Mismatches
                                                                                  7 QLEHRERSLQTLRDIQRMLFPDEKEFT 33
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-186-276B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 VQQSRIQHLEQSLERLQDRERRL 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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LENGTH: 524
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                      Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Best Local Similarity
Matches 10; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-32259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM:
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Job time : 9.08171 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

October 15, 2003, 10:32:06; Search time 14.8444 Seconds (without alignments) 379.908 Million cell updates/sec Run on:

US-09-915-543-15_COPY_349_383 178 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35

Title: Perfect score: Sequence:

BLOSUM62 Cabop 10.0 , Gapext 0.5 Scoring table:

600653 seqs, 161128416 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

Published_Applications_AA:*

| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 5, Appli	Sequence 15, Appl	Sequence 17, Appl	Sequence 4, Appli	Sequence 3511, Ap	Sequence 8511, Ap	Sequence 12, Appl	Sequence 32, Appl	Sequence 21, Appl	Sequence 30, Appl	Sequence 31, Appl	14,	Sequence 16, Appl	Sequence 19, Appl	Sequence 18, Appl
	ΩI	US-10-322-579-5	US-10-322-579-15	US-10-322-579-17	US-10-322-579-4	US-10-128-714-3511	US-10-128-714-8511	US-10-053-248-12	US-10-284-753-32	US-10-097-340-21	US-10-284-753-30	US-10-284-753-31	US-10-097-340-14	US-10-097-340-16	US-10-097-340-19	US-10-097-340-18
	DB	15	15	15	15	15	15	12	16	15	16	16	15	15	15	15
	Query Match Length D	35	1426	1115	35	603	618	294	333	390	433	433	464	643	718	751
d	Query Match	100.0	100.0	60.1	37,1	32.3	32.3	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9
	Score	178	178	107	99	57.5	57.5	55	55	55	55	55	55	55	55	52
	Result No.		7	æ	4	Ω.	9	7	œ	6	10	11	12	13	14	15

Sequence 4987, Ap Sequence 10651, A Sequence 466, App Sequence 466, App Sequence 4366, App	Sequence 11828, A Sequence 119, App Sequence 28, Appl Sequence 2, Appli	Sequence 323, App Sequence 24, Appl Sequence 56, Appl Sequence 306, Appl	Sequence 86, Appl Sequence 8, Appl Sequence 29, Appl Sequence 277, Appl	Sequence 15, Apples Sequence 14821, A Sequence 11081, A Sequence 10420, A Sequence 63, Appl	Sequence 3, Appli Sequence 8235, Ap Sequence 3235, Ap Sequence 5, Appli Sequence 2062, Ap Sequence 14264, A Sequence 12, Appl
9 US-09-815-242-4987 9 US-09-815-242-10651 10 US-09-731-872-466 12 US-09-876-997-466 10 US-09-738-626-4366	9 US-09-815-242-11828 12 US-10-161-051-119 12 US-10-236-055A-28 15 US-10-227-610-2	15 US-10-043-487-323 15 US-10-234-432-24 15 US-10-253-007-56 15 US-10-043-487-306	15 US-10-234-432-86 12 US-09-840-743-8 13 US-10-010-901-29 15 US-10-043-487-277		11 US-09-298-523B-3 15 US-10-128-714-8235 15 US-10-128-714-3235 11 US-09-819-104A-5 9 US-09-867-550-2062 15 US-10-156-761-14264 14 US-10-062-254-12 9 US-09-864-761-42510
444 500 500 544	1162 464 804 2654	2001 4001 4001 5001	893 1413 2000 898	170 182 861 529 670	711 810 841 2462 100 118 139
28.7 28.7 28.7 28.7	28.1 27.8 27.8 27.8	22 22 22 23 25 25 25 25 25	27.5	27.0 27.0 26.7 26.4 26.4	2222222 222222 202222 44441888
51 51 50 50	49.5 49.5 49.5	4444 9000	4 4 9 9 9 9 9 9 9	48 47.5 47 47	4 4 6.4 7 7 4 4 6 6 6 6
16 17 18 19 20	2 2 2 2 2 2 2 2 4 3 5 4	2265 2265 2465	20 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8 4 6 8 6	8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Sequence 5. Application US/1032579

Sequence 5. Application US/10322579

Publication No. US2003011441341

GENERAL INFORMATION:

APPLICANT: BASIER, Konrad

APPLICANT: REMARS, Thomas

APPLICANT: FROESCH, Barbara

APPLICANT: FREME, Oliver

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

TITLE OF INVENTION: UNMBER: US/10/322,579

CURRENT FILING DATE: 2001-07-27

PRIOR PILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PALENTIN VETSION 3.1

SEQ ID NO 5

LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
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US-10-322-579-5
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Best Local Similarity
Matches 35; Conserv
RESULT 1
US-10-322-579-5
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RESULT 2 US-10-322-579-15

Wed Oct 15 11:40:28 2003

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Webult 3

Wellication Wo. US203011901341

Sequence 351, Application US/10128714

Publication No. US203011901341

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Tishkoff, Daniel

APPLICANT: Tishkoff, Daniel

APPLICANT: Eroshkin, Alexey M

APPLICANT: Eroshkin, Alexey M

APPLICANT: Lamdio, Carlos

APPLICANT: Lamdio, Carlos

FULTE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and TITLE OF INVENTION: Methods of Use

FILE REPERBYCE: 1012-018-99

CURRENT PLIANG DATE: 2002-04-23

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SOUTHARE: PATENTIN OFFICE OFFI
publication No. US20030114413A1

GENERAL INFORMATION:
APPLICANT: BASLER, Konrad
APPLICANT: BASLER, Konrad
APPLICANT: BASLER, Enich
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Thomas
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH)
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH)
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH)
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH)
FILE REFERENCE: 060361
CURRENT FILING DATE: 2002-12-19
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 05/221,502
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.1%; Score 66; DB 15; Length 35; ilarity 31.4%; Pred. No. 0.05; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.48
Matches 11; Conservative
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US-10-322-579-4
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Matches 11; Conser
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LENGTH: 35
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                                                                                                                                                                                                                                                       ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
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Pred. No. 8.1e-06;
3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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llarity 100.0%; Pred. No. 3.2e-15;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/10322579;
Sequence 17, Application US/10322579;
Publication No. US20030114413A1
GENERAL INFORMATION:
APPLICANT: BASLER, Konrad
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: KRAMPS, Thomas
APPLICANT: KRAMPS, Thomas
APPLICANT: FROESCH, Barbara
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COM;
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COM;
FILE REFERENCE: Q60361
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
                                                                                           APPLICANT: BRUNNER, Erich
APPLICANT: BRUNNER, Erich
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, BARBARA
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM CO
TITLE OF INVENTION: THERAPEUTIC AND DIAGN
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                           NUMBER: US/10/322,579
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         Sequence 15, Application US/10322579 Publication No. US20030114413A1 GENERAL INFORMATION:
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ervative 3
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US-10-322-579-15
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US-10-322-579-17
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Best Local Similarity
Matches 35; Conserv
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SOFTWARE: Patentin
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simil
Matches 21; (
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TYPE: PRT
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US-10-322-579-17
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US-10-322-579-4
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Peter VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
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Karen GLATT
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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            RESULT 8
US-10-284-753-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 618;
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Pred. No. 17;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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## APPLICANT: Lin, Biacyang
## TITLE OF INVENTION: Androgen Regulated Nucleic Acid
## TITLE OF INVENTION: Molecules and Encoded Proteins
## TITLE OF INVENTION: Molecules and Encoded Proteins
## FILE REFERENCE: P-IS 4814
## CURRENT APPLICATION NUMBER: US/10/053,248
## CURRENT FILING DATE: 2002-01-15
## SOFTWARE: FastSEQ for Windows Version 4.0
## SOFTWARE: FastSEQ for Windows Version 4.0
## SOFTWARE: PRI
## TYPE: PRI
## ORGANISM: Homo Sapiens
## US-10-053-248-12
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DGVETEKIREKD --- EVEKKLERMLFGDDEGFVGA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Aspergillus fumigatus US-10-128-714-8511
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ilarity 52.2%;
Conservative 4
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Best Local Similarity
Matches 12; Conserv
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US-10-053-248-12
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                                                                                                                                                                                                               DB 15; Length 390;
23;
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                                                                                                                                                                                                                                Query Match 30.9%; Score 55; DB Best Local Similarity 52.2%; Pred. No. 23; Matches 12; Conservative 4; Mismatches
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; Sequence 31, Application US/10284753
; Publication No. US20030129655A1
; GENERAL INFORMATION:
; APPLICANT: Kiinger, Tod M.
; APPLICANT: Stewart, Elizabeth A.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: GTPASE ACTIVATING PROTEI:
FILE REFERENCE: PC-0010-1 CIP
; CURRENT APPLICATION NUMBER: US/10/284,753
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/507,765
; PRIOR FILING DATE: 2000-02-18
; SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stewart, Elizabeth A.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEI
FILE REFERENCE: PC-0010-1 CIP
CURRENT APPLICATION NUMBER: US/10/284,753
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/507,765
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 30
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 390
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-097-340-21
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CTHER INFORMATION:
US-10-284-753-30
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US-10-284-753-30
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US-10-284-753-31
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APPLICANY: AMI SEN
APPLICANY: Peter VEIBY
APPLICANY: Peter VEIBY
APPLICANY: Poter VEIBY
APPLICANY: Roles MILLS
APPLICANY: Robert C. BAST, Jr.
APPLICANY: Raren Lu
APPLICANY: Raren Lu
APPLICANY: Raren Li
APPLICANY: Karen Li
APPLICANY: Karen GLATT
APPLICANY: MUBBER: 60/216,025
APPLICANY: MUBBER: 60/216,025
APPLICANY: MUBBER: 60/216,026
APRIOR FILING DATE: 2001-03-14
APPLICANION NUBBER: 60/216,026
APRIOR FILING DATE: 2001-03-14
APPLICANION NUBBER: 60/311,732
APRIOR FILING DATE: 2001-09-19
APRIOR APPLICANION NUBBER: 60/311,732
APRIOR APPLICANION NUBBER: 60/311,732
APRIOR APPLICANION NUBBER: 60/313,736
APPLICANION NUBBER: 60/323,580
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APPLICANION 
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O
                                                                                      NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. US20030129655A1 404424.5.pseq US-10-284-753-31
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Pred. No. 28;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                             Length 433;
                                                                                                                                                                                                                                                                                                                                7; Indels
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52.2%; Pred. No. 26;
live 4; Mismatches 7
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APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
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52.2%;
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Best Local Similarity 52.2'
Matches 12; Conservative
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US-10-097-340-14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 12; Conserve
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Sequence 18, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
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APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
Rosemarie SCHMANDT
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Robert C. BAST, Jr.
Karen LU
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Xumei ZHAO
Karen GLATT
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Best Local Similarity !
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Karen GLATT
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                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOYARS
APPLICANT: Rachel E. METERS
APPLICANT: Redel E. METERS
APPLICANT: Reder CLANDT
APPLICANT: Robert C. BAST, JT.
APPLICANT: Robert C. BAST, JT.
APPLICANT: Main is ElMO
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US-10-097-340-19
; Sequence 19, Application US/10097340
; Publication No. US20030087250Al
; GENERAL INFORMATION:
                               RESULT 13
US-10-097-340-16
; Sequence 16, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
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APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Peter OLANDT
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
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US-10-097-340-16
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NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserv
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TITLE OF INVENTION: Nacial Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR PRICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PRILING DATE: 2001-09-36
PRIOR APPLICATION NUMBER: 60/325,60
PRIOR APPLICATION NUMBER: 60/325,60
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-18
PRIOR PRILING DATE: 2001-09-18
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52.2%; Pred. No. 4,,
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
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PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001/09/26

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-18

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-18

CONGRAINMENT PATE

PRIOR FILING DATE: 2001-09-34

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-34

PRIOR
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Search completed: October 15, 2003, 10:50:58 Job time: 15.8444 secs

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Compugen Ltd.
 version - 2003
GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

(without alignments)
405.170 Million cell updates/sec 2003, 10:27:32 ; Search time 8.30739 Seconds 15, October Run on:

US-09-915-543-15_COPY_349_383 178 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 96168682 residues 283308 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution. Pred. No. is the score greater than and is derived by

STIMMARTES

	Description	exonuclease SbcC [a)		transcription regu	hex regulon repres	act	ochrome B	protein -	ALR protein - huma	hypothetical prote	gamma-D-glutamyl-L	mismatch DNA recog		_	phytochrome B - so	probable transcrip	transcription init	pyruvate dehydroge	hypothetical prote	i hypot	probable alpha hel	probable alpha hel					ATP-dependent dsDN	ATP-dependent dsDN	development protei
SUMMARIES	er er	AB05	S51882	T4637	AE289	H9767	B59			T0345			S62790										E3			-	Ö	G9068	C85	S2
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	& Query Match Length	1034	584	859	287	295	643	1171	4957	5262	227	376	818	242	705	1039	332	332	572	1009				237	329	477	899	1047	1047	1464
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AD2441 H69337	H69843 S49771	G86454 S67595	D83454	B50329 AE1124	TPCHTC S72858	T18860	A84142	E81730	T41236	C90796
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30 31	332	9.60 4.70	36	3.7 3.8	39 40	4.1	42	43	44	45

ALIGNMENTS

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excunciesse SDCC [imported] - Salmonella enterica subsp. enterica serovar Typhi (str. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AB0551
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, A;Itile: Complete genome sequence of a multiple drug resistant Salmonella enterica si A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Scession: AB0551
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL513382; PIDN:CAD08850.1; PID:g16501663; GSPDB:GN00176
C;Genetics:
A;Gene: STY0429
C;Superfamily: sbcC protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein HRC584; protein 00716; protein YOL115w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000
C;Accession: S51882; S59158; S58774; S66811
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV incluand a Delta.
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A; Reference number: S51848
A; Accession: S51882
A; Molecule type: DNA
A; Residues: 1-584 <VAN>
A; Residues: 1-584 <VAN>
A; Cross-references: EMBL: Z48149; NID: 9663234; PID: 9663237
B; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A; Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including a delta element.
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Best Local Similarity 42.9%;
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hex regulon repressor [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Accession: H97670
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldn A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; MUID:21608551; PMID:11743194
   ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
                                                                                                                   ster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Accession: AE2895
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-287 < KUR>
A; Residues: 1-287 < KUR
A; Residues:
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Rho GrPase activating protein RhoGAP8 - human
C; Species: Homo sapiens (man)
C; Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 23-Sep-2002
C; Accession: B59436
R; Goward, M.E.; Huckle, E.J.
submitted to GenBank, April 2000
A; Reference number: B59436
A; Reference number: B59436
A; Accession: B59436
A; Accession: B59436
A; Accession: B59436
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-643 <GOW>
A; Residues: 1-643 <GOW>
A; Cross-references: GB:CAB90248; PID:g7711011; PIDN:CAB90248.1
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QQRQRSMVTLRHIKQQLVEHRDPDDKQLLG 294
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QQRQRSMVTLRHIKQQLVEHRDPDDKQLLG 286
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55;
Pred. No. 1
7; Mismatch
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No.
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Pred. No.
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A;Map position: circular chromosome
C;Superfamily: hypothetical protein ybbH
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Pred.
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52.2%;
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A;Molecule type: DNA
A;Residues: 1-295 <KUR>
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Best Local Similarity
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nes 12; Conserv
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                                                                         A.Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-584 <VAW>
A;Residues: 1-584 <VAW>
A;Cross-references: EMBL: 248149; NID: 9662334; PIDN: CAA88145.1; PID: 9663237
A;Orte: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Title: Lisolation of mutants of Saccharomyces cerevisiae requiring DNA topoisomerase I.
A;Reference number: S58774; MUID: 96109595; PMID: 8647385
A;Accession: S58774; MUID: 96109595; PMID: 8647385
A;Cross-references: EMBL: U31355; NID: 9950225; PIDN: AAC49091.1; PID: 9950226
B;Durand, P.: Hilger, F.: Portetelle, D.: Vandenbol, M.
A;Residues: 1-584 <SAD>
A;Cross-reference number: S66791
A;Recence number: S66791
A;Recence number: S66791
A;Residues: 1-584 <DNA
A;Residues: 1-584 <DN
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C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: AE2895
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C; Accession: T46372
R; Ottenwaelder, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R; Ottenwaelder, B.; Dermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R; Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R; Ottenwaelter, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R; Reference number: Z23031
A; Reference number: Z
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   )156; MUID:96076631; PMID:7502582
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Best Local Similarity 33.3°
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Best Local Similarity
Matches 9; Conser
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A;Experimental source:
C;Genetics:
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A;Map position: 15L
C;Keywords: nucleus
   number:
                                                    A; Accession: S59158
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Gene: SGD:TRF4
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A;Reference
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dosep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E69957
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be.
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Ga
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, J.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mai
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mai
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Seato, T.; Scan
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sekwaska, A.; Scan
A;Authors: Schleich, S.; Schroeter, R.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyell, M.; Tamakoshi, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000747; NID:g2983944; PIDN:AAC07503.1; PID:g2983955; GB:AE0 C;Genetics: A;Gene: aq_1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
B70438
hypothetical protein ag_1596 - Aquifex aeolicus
C; Species: Aquifex aeolicus
C; Species: Aquifex aeolicus
C; Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C; Accession: B70438
R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E. V.
Nature 392, 353-358, 1998
A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID: 98196666; PMID: 9537320
A; Accession: B70438
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-227 <AQF>
                                                                                                     strong hom-
                                            T.; Rallapalli,
                                                                                                                                                                                                                                                                           PID:92358285
                                                                                                   gene with
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C; Accession: T03454
R; Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Oncogene 15, 549-560, 1997
Oncogene 15, 549-560, 1997
A; Title: Structure and expression pattern of human ALR, a novel ge A; Reference number: 214954; MUID: 97388474; PMID: 9247308
A; Accession: T03454
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-5262 <PRA>
A; Residues: 1-5262 <PRA>
A; Cross-references: EMBL: AF010403; NID: 92358284; PIDN: AAC51734.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5262;
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Pred. No. 4.5e+02;
; Mismatches 12;
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Best Local Similarity 42.5%;
Matches 17; Conservative
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C:Superfamily: human ALR protein
C: Keywords: alternative splicing
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Best Local Similarity
Watches 12; Conserv
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                                                                                                                                                                                                                                                              phytochrome B - rice
C; Species: Oryza sativa (rice)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
C; Accession: S14065
R; Dehesh, K.; Tepperman, J.; Christensen, A.H.; Quail, P.H.
Mol. Gen. Genet. 225, 305-313, 1991
A; Title: phyB is evolutionarily conserved and constitutively expressed in rice seedling
A; Reference number: S14065; MUID: 91172131; PMID: 2005872
A; Accession: S14065
A; Satus: preliminary
A; Moluelle type: DNA
A; Residues: 1-1171 ADEH>
A; Cross-references: GB: X57563; NID: 96469490; PIDN: CAA40795.2; PID: 96469491
C; Genetics:
A; Generics:
A; Genericanily: phytochrome homology
C; Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
F; 103-623/Domain: phytochrome homology <PHYT>
F; 364/Binding site: phytochromeobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel gene with strong homolog
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C.Sacession: T03455
R.Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.;
Oncogene 15, 549-560, 1997
A.Title: Structure and expression pattern of human ALR, a novel gene with strong hc
A; Reference number: Z14954; MUID:97388474; PMID:9247308
A; Reference number: Z14954; MUID:9738866; PIDN:AAC51735.1; PID:92358287
A; Ross-references: EMBL:AF010404; NID:92358286; PIDN:AAC51735.1; PID:92358287
C; Genetics:
A; Genetics:
A; Map position: 12
C; Superfamily: human ALR protein
C; Keywords: alternative splicing
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ALR protein - human
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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Pred. No. 4.3e+02;
I; Mismatches 12;
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Pred. No. 63;
4; Mismatches
                   Mismatches
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GLRTEGLFRRSASVQTVREIQRL 456
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Best Local Similarity 42.5%;
Matches 17; Conservative
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                   Conservative
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                   12;
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C;Superfamily: Aquifex aeolicus hypothetical protein aq_755
                                                   Query Match 29.5%;
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                             hypothetical protein T02B5.1
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A; Accession: T14802
A; Status: preliminary: trar
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Best Local S
Matches 14
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S62790
mismatch DNA recognition protein mutS [validated] - Thermus aquaticus (fragment)
C; Species: Thermus aquaticus
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C; Accession: S62790
R; Takamatcu, S.; Kato, R.; Kuramitsu, S.
Nucleic Acids Res. 24, 640-647, 1996
A; Title: Mismatch DNA recognition protein from an extremely thermophilic bacterium, Ther A; Reference number: S62790; MUID:96177563; PMID:8604304
A; Reference number: S62790
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-ype: DNA
A; Residues: 1-ype: DNA
A; Residues: 1-ype: DNA
A; Note: the source is designated as Thermus thermophilus
C; Genetics:
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A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID: 98044033; PMID: 9384377
A; Accession: E69957
A; Accession: E69957
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-376 < KUN>
A; Experimental source: GB: Z99116; GB: AL009126; NID: 92634723; PIDN: CAB14414.1; PID: 92634917
A; Experimental source: strain 168
C; Genetics:
A; Gene: YggT
C; Superfamily: endopeptidase I
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000
C;Accession: B70366
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graf
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Pred. No. 67;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                 Score 53; DB Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 EHSGKELQTIQDIKRFLQP 68
                                                                                                                                                                                                                                                                                                                                                                                                                               EHRERSLQTLRDIQRMLFP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.8%;
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                 29.8%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 392, 353-358, 199
A; Title: The complete ge
A; Reference number: A703
A; Accession: B70366
A; Status: preliminary; n
A; Molecule type: DNA
A; Residues: 1-242 <AQF>
A; Cross-references: GB:A
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVPQEYR
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C; Genetics:
A; Gene: aq_755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
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C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
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phytochrome B - sorghum (fragment)
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14802
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mul]
submitted to the EMBL Data Library, April 1996
A;Description: The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phyto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: T24343
R; McMurray, A.
submitted to the EMBL Data Library, October 1996
A; Reference number: 219878
A; Molecule type: DNA
A; Residues: 1-705 < WWIL>
A; Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ;
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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A;Residues: 1-1039 <CHI>
A;Cross-references: EMBL:U56730; NID:91800216; PID:91800217
A;Experimental source: cultivar 58M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 LSEEQVENTYSCLRKKSAQQILDAQLWLLQNSTYFLGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LSQEQLEH----RERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52.5; DB 2;
Pred. No. 1e+02;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Score 52.5; Di
Pred. No. 20;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 29.5%; Score 52.5; D
Local Similarity 36.8%; Pred. No. 66;
les 14; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LSQEQLEHRERSLQTLRDIQRMLFPDE 29
                                                                                                                                                                                              10 HRERSLQT-LRDIQRMLFPDEKEF
                                                                                                                                                                                                                                                   60 HKRTSLRKFVREIEKMVFEAEKEF
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Best Local Similarity 51.9%;
Matches 14; Conservative
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Search completed: October 15, 2003, 10:33:10 Job time: 11.3074 secs

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5.1.6
Compugen Ltd
version - 2003
GenCore
Copyright (c) 1993
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- protein search, using sw model OM protein

(without alignments)
389.867 Million cell updates/sec ; Search time 4.22179 Seconds 2003, 10:27:32 15, October Run on:

15-543-15_COPY_349_383

EQLEHRERSLQTLRDIQRMLFPDEKEFTGA US-09-9: 178 1 DGLSQ Title: Perfect score: Sequence:

32 10.0 , Gapext 0.5 BLOSUM6 Gapop 1 Scoring table:

seqs, 47026705 residues 127863 Searched: 127863 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

um Match 0% Post-processing: Minimu

Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	nescraption	~1	<u> </u>	~;			മാനായ വ		bac111us	thermus								Q06407 saccharomyc			Q9cxp4 mus musculu	Q92794 homo sapien	_	_							,	P29130 nicotiana t		P21675 homo sapien
SUMMARIES	í,	1D	BCL9_HUMAN	BCL9_DROME	TRF4_YEAST	HEM1_SYNEL	RHG8_HUMAN	ASH3_MOUSE	PHYB_ORYSA	YQGT_BACSU	MUTS_THECA	MUTS_THETH	ASH3_HUMAN	RRF_FUSNN	Y755_AQUAE	PHYB_SORBI	RPSB_ANASP	MUTS_THEAQ	RGA2_YEAST	YFHG_ECOLI	POL MMTVB	RHG8_MOUSE	MOZ_HUMAN	TRT2_CHICK	DYN1_CAEEL	LDH_BACHD	PLSX_STAAW	YDBJ_SCHPO	DML1_ARATH	PIP3_HUMAN	YWKC_BACSU	CARB_METMA		SCP2_RAT	T2D1_HUMAN
	5		٦	~	Н	-	,	_	1																								<u>, , , , , , , , , , , , , , , , , , , </u>		
	1	Length	42	1469	584	426	718	174	1171	376	817	818	180	190	242	1178	332	811	1009	237	899	425	2004	301	830	310	328	661	1207	1234	184	1073	1132	1505	1872
đ	Query	Match	100.0	37.1	31.5	30.9	30.9	30.6	30.6	29.8	29.8	29.8	29.5	29.5	29.5	29.5	29.5	29.5	29.5	28.7	28.7	28.1	28.1	27.8	27.8	27.5	27.5	27.5	27.5	27.5	27.2	27.2	27.2	27.2	27.2
		score	178	99	56	55	55	4	•	53	53	53				52.5		52	52	51	51	20	50		σ	49	49	49	49	49		∞	48.5		
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Q99un9 staphylococ P34934 sus scrofa P47040 saccharomyc Q08032 saccharomyc P43439 enterococcu O02849 ovis aries Q8tvb2 methanopyru P53059 saccharomyc P44834 haemophilus Q8ra24 thermoanaer P58790 agrobacteri	
1 PLSX_STAAM 1 HS7X_PIG 1 BTN1_YEAST 1 CC45_YEAST 1 NTPI_ENTHR 1 PDI3_SHEEP 1 PYRB_METKA 1 MNT2_YEAST 1 MUTS_HAEIN 1 RRF_THETN 1 HIS4_AGRT5	1 HSLO_BACST
328 379 408 664 664 309 1861 184	296
27.0 27.0 27.0 27.0 27.0 26.7 26.7 26.7 26.7	26.4
44444444444444444444444444444444444444	47
88888884444 48868884444	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21952490; PubMed=11955446;

MEDLINE=21952490; PubMed=11955446;

MITCHER TO., Brunner E., Nellen D., Froesch B., Chatterjee S., Mirche M., Zuellig S., Basler K.;

Murone M., Zuellig S., Basler K.;

Cell 109:47-60(2002).

Cell 109:47-60(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignancies.
CAUTION: It is uncertain whether Met-1 or Met-27 is the initiator.
CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal brain;
MEDLINE=98158621; PubMed=9490669;
Willis T.G., Zalcberg I.R., Coignet L.J.A., Wlodarska I., Stul M.,
Jadayel D.M., Bastard C., Treleaven J.G., Catovsky D., Silva M.L.M.,
Dyer M.J.S.;
"Molecular cloning of translocation t(1;14)(q21;q32) defines a novel
gene (BCL9) at chromosome 1q21.";
Blood 91:1873-1881(1998).
                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
B-cell lymphoma 9 protein (Bcl-9) (Legless homolog).
                                                          1426 AA
                                                          PRT;
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
RESULT
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us-09-915-543-15_copy_349_383.rsp

δ

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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAY Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Hill R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Hill R.A., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Garder S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Tandell M.D., Zhang O., Chen L.X., Stutton G.G., Wortman J.R., The College M., Pfeiffer B.D., R.A. Brandon R.C., Ragavani A., An H.J., Andrews Pfannkoch C.P., Baddwin D., Radlew R.M., Basu A., Barnen B.P., Bandari D., Bolshakov S., Ballew R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I., Reson M.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S., Rorkova D., Botchan M.R., Boutk J., Markels B.C., Davreport L.B., Dottler P., Botchan M.R., Boutk J., Markels B.C., Davreport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Dett S.M., Achery J.M., Markel M.B., Markel M.P., Sahle B., Mount S.M., Moy M., Murphy B., Murphy L., Mazny D.M., Nelson D.L., Radington M., Stupski M.P., Sahlth T., Radington M., Stupski M.P., Sahlth T., Radington M., Stupski M.P., Sahlth T., Radington M., Stubsken D.R., Washer M. Sture R., Spier E., Spier E., Stapleton M., Stubsken D.T., Wang X., Radington M., Stubski M.P., Sahlth T., Radington M., Weinsten R., Weissenbach J., Radingtock G., Turner R., Weissenbach J., Wang X., Tector C., Turner R., Weissen B. J., Weissen B., We
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                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaster (Fruit fly).
a; Arthropoda; Hexapoda; Insecta; Pterygota;
rygota; Diptera; Brachycera; Muscomorpha;
ophilidae; Drosophila.
                                                                                                                                                                                                                           Length 1426;
                                                             Nuclear protein; Chromosomal translocation; Proto-oncogene; Whit signaling pathway.

DOMAIN 231 1378 PRO-RICH.

DOMAIN 347 377 CTNNB1-BINDING.

DOMAIN 331 335 POLY-PRO 1.

DOMAIN 514 517 POLY-PRO 2.

DOMAIN 900 903 POLY-PRO 2.

DOMAIN 970 973 POLY-PRO 3.

SEQUENCE 1426 AA; 149314 MW; A240A487716B7F1B CRC64;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         100.0%; Score 178; DB 1;
100.0%; Pred. No. 3.1e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                        41, Created)
41, Last sequence update)
42, Last annotation update)
gless protein).
                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1469 AA
 EMBL; Y13620; CAA73942.1; ALT_FRAME.
Genew; HGNC:1008; BCL9.
MIM; 602597; -.
GO; GO:0007048; P:oncogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10731132;
                                                                                                                                                                                                                                                             rvative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         BCL9_DROME STAN
Q961D9; Q9V4D2;
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
15-SEP-2003 (Rel. 4
BCl-9 homolog (Leg1
BCL9 OR LGS OR CG2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanoga
Eukaryota; Metazoa;
Neoptera; Endoptery
Ephydroidea; Drosop
NCBL_TaxID=7227;
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Berkeley; MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                          349
                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
BCL9_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003844; AAF59345.1; ALT_SEQ.

R EMBL; AX051651; AAK93075.1; -.

R EMBL; AX651651; AAK93075.1; -.

R EMBL; Ax457205; AAL91368.1; -.

R EMBL; Ax457205; AAL9136.1; -.

R EMBL; Ax457205; AAL9136.1; -.

R EMBL; Ax457205; AAL9136.1; -.

R GO; GO:0005634; C:nucleus; IEP.

R GO; GO:000634; C:nucleus; IEP.

R GO; GO:0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21952490; PubMed=11955446;

Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.;

Murone M., Zuellig S., Basler K.;

Murone M., Zuellig S., Basler K.;

"Wnt/wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";

Cell 109:47-60(2002).

-!- FUNCTION: Involved in signal transduction through the wnt pathway.

C.!- SUBCELLULAR LOCATION: Nuclear.

-!- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 6-1469 FROM N.A., AND MUTAGENESIS OF GLY-514; LEU-534 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35
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1469 AA;
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ID TRF4_YEAST
AC P53632;
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                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                     statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                               suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and a delta element.";
Yeast 11:1069-1075(1995).
-!- FUNCTION: ESSENTIAL PROTEIN REQUIRED FOR PROPER NUCLEAR DIVISION IN MITOSIS. MAY MEDIATE MITOTIC CHROMOSOME CONDENSATION.
-!- SIMILARITY: BELONGS TO THE CID1/TRF4/TRF5 FAMILY.
                                                                                                                                                                                                                                                       Vandenbol M., Durand P., Portetelle D., Hilger F.; "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Tyl-H3 retrotransposon, the sufl(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and a
                                                                                                                           MEDLINE-96109595; PubMed-8647385;
Sadoff B.U., Heath-Pagliuso S., Castano I.B., Zhu Y., Kieff F.S.
Christman M.F.;
                                                                             Saccharomycetes;
                                                                                                                                                                             "Isolation of mutants of Saccharomyces cerevisiae requiring DNA topoisomerase I.";
Genetics 141:465-479(1995).
[2]
SEQUENCE FROM N.A.
MEDLINE-96076631; PubMed=7502582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :nucleus; IDA.
:DNA-directed DNA polymerase activity; IDA.
:DNA topological change; IGI.
:mitotic chromosome condensation; IMP.
:34; NTP_transf.
:01; PAP_25A_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 1; Length 584;
Pred. No. 8.7;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66030 MW; 8A58B29E4BFDC022 CRC64;
                                                                          Ascomycota; Saccharomycotina; Sacc
Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEM1_SYNEL STANDARD; PRT; 426 AA. Q8D153; 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR). HEMA OR TLL1738.
 34, Created)
34, Last sequence update)
40, Last annotation update)
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update
16-OCT-2001 (Rel. 40, Last annotation update
Topoisomerase 1-related protein TRF4.
TRF4 OR YOL115W OR O0716 OR HRC584.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: |:|: |:|| NQTISTIREAVKQLWPD 217
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36.0%;
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                                                                             Eukaryota; Fungi;
Saccharomycetales;
NCBI_TaxID=4932;
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Matches 9
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or send a
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                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=BP-1;

MEDLINE=22225144; PubMed=12240834;

Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

Nakamura Y., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

RA Watsunobe A., Iriguchi M., Takeuchi C., Yamada M., Tabata S.;

RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT Complete genome structure of the thermophilic cyanobacterium

RT Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

CC -!- CATALYTIC ACTIVITY: Glutamyl-tRNA(Glu) + NADPH = glutamate-1-

Semialdehyde + NADP(+) + tRNA(Glu).

CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.

Involved in chlorophyll biosynthesis.

CC -!- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.

CC -!- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
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InterPro; IPR000343; GlutR.
InterPro; IPR000594; ThiF_domain.
Pfam; PF00745; GlutR_dimer; 1.
Pfam; PF05201; GlutR_N; 1.
Pfam; PF05200; GlutR_NaD_bind; 1.
TIGRFAMS; TIGR01035; hema; 1.
PROSITE; PS00747; GLUTR; FALSE_NEG.
Porphyrin biosynthesis; Chlorophyll biosynthesis; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 4).

Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,

Yu J., Han L.H.;

"Novel human cDNA clone with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHG8 HUMAN STANDARD; PRT; 718 AA.
Q9NSG0; 075983; 095695; Q96RW1; Q96RW2; Q9HA49; Q9HC46; Q9NVX8;
Q9NXL1; Q9UH20;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rho-GTPase-activating protein 8.
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Pred. No. 8.2;
5; Mismatches 3; Indels
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BASE (BY SIMILARITY).
D84CE5AlD2AA777E CRC64;
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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SQRDLESRQRAMQTLQDL 418
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47596 MW;
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Best Local Similarity 55.6%;
Matches 10; Conservative 9
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detected are isoforms 1 to 7. Experimental confirmation may

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RR PGDENCE FROM N.A.

RA PEDIANE-2005165; PubMed-10591208;

RA PEDIANE-2005165; PubMed-10591208;

RA BAGGULGV C., Balley J., Ballow K.P., Bares K.W., Beastey O.P.,

RA BAGGULGV C., Balley J., Barllow K.P., Bares K.W., Beastey O.P.,

RA BLIG C.P., Black S.E., Barddeman A.M., Buck D., Burgess J.P.,

RA BLIG C.P., Black S.E., Barddeman A.M., Buck D., Burgess J.P.,

RA BLIG C.P., Black V.E., Cole C.G., Collier R.E., Connor R.,

COUTOY D., CODREY V.E., COLOSING S.J., DULDIN R.M., Ellington A.G.,

RA Glibert J.G.R., Goward M.E., French L., Garner A.A.

RA Glibert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathortort R.W., Ho S., Holmes S.,

RA Hall R.E., Jones M.C., Kershaw J., Kinnberley A.M., King A.,

Laird G.K., Langford C.F., Leversta M.A., King A.,

RA Martyn I.D., Washreghi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Washreghi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Washreghi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Walliams S.H., Plumb R.W., Ramsay H., Ransey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sepragon L., Steward C.A., Suiston J.E., Swann R.M.,

RA Williams L., Williams S.A., Williams S.,

RA Scott C.L., Hubbard T., Bearley D.R., Willer T.E., Wilming L.,

Williams L., Williams S.A., Williams S., Rawasaki R., Walliamson H., Willer Y. Borman S.,

Roren B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kaudoh J.,

RA Minoshima S., Shibuya K., Yoshizaki Y., Asakawa S., Kaudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Asakawa S., Rogers S., Mannon A., Eng S., Lin S.-P., Loh P., Malaj E., Najulian T., Pah R.,

RA Shintani A., Shibuya K., Yoshizaki Y., Asakawa S., Banteson S., Mall Son J.,

RA Phan S., Ola S., John Y., Buya A., Walliands M., Millow R., Wang C., Manz Y., Wang C., Multer J., Waller D., Waller 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              them to an inactive GDP-bound state (By similarity).

Event=Alternative splicing; Named in Comment=Additional
                                                                                            SEQUENCE FROM N.A. (ISOFORMS 5; 6 AND 7).

SEQUENCE FROM N.A. (ISOFORMS 5; 6 AND 7).

ISSUE=Colon mucosa, and Mammary gland;
ISOGai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

"NEDO human CDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                     chromosome 22q13.3."; databases.
                                                                                                                                                                                                                                                                                       1e E.J.;
00) to the EMBL/GenBank/DDBJ databases
to the EMBL/GenBank/DDBJ databases
             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
McDermid H.E., Hu S., Grundy P., Trichet V.;
*ARHGAP8: a putative tumor-suppressor gene on
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                       (ISOFORM 3).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Goward M.E., Huckle Submitted (APR-2000[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilkinson P., Bod
Tilahun Y., Wrigh
"The DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LORDKAAAAAVLGAVRKRPSVVPMAGQDPALSTSHPFYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHGILQVAGDDRFGRRVVTFSCCRMPPSHELDHQRLLEYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTLDOYVENDYTIVYFHYGLNSRNKPSLGWLQSAYKEFDRK
DGDLTMWPRLVSNSKLKRSSHLSLPKYWDYRYKK -> KRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRRSRSGDVLAKNPVVRSKSYNTPLLNPVQEHEAEGAAAGG
TSIRRHSVSEMTSCPEPQGFSDPPGQGPTGTFRSSPAPHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCPSRLYPTTQPPEQGLDPTRSSLPRSSPENLVDQILESVD
SDSEGIFIDFGRGRGSGMSDLEGSGGRQSVV (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (In isoform 1 and isoform 2). /FTId-VSP_001649.
                                                                                                 VSP_001649, VSP_001652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9NSG0-8; Sequence=VSP_001646, VSP_001648, VSP_001650, VSP_1001654; SIMILARITY: Contains 1 CRAL-TRIO domain. SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                              IsoId=09NSG0-7; Sequence=VSP_001647, VSP_001652, VSP_001656, VSP_01656,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                     VSP_001649, VSP_001653,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 5 and isoform /FTId=VSP_001647.
KIRFYE -> MAPMPT (in isoform 7).
/FTId=VSP_001648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 1 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoform 4 and isoform 7).
                                                                                                                                                                                                                                                                                Sequence=VSP_001650, VSP_001654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_001645.
Missing (in isoform 7).
/FTId=VSP_001646.
                                                                                                                                                   Sequence=VSP_001645,
                                                                                                                                                                                                                                                                                                            ISOId=09NSG0-6; Sequence=VSP_001647;
Name=6;
                                                                                                                                                                                                         Name=3;
IsoId=Q9NSG0-4; Sequence=VSP_001651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTPase activation; Alternative splicing.
DOMAIN 267 453 CRAL-TRIO.
DOMAIN 480 666 RHO-GAP.
VARSPLIC 1 95 Missing (in
                                                   IsoId=Q9NSG0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF177331; AAG17975.1; -.
EMBL; AF195968; AAK58136.1; -.
EMBL; AF195969; BAAK58137.1; -.
EMBL; AK00192; BAA90999.1; -.
EMBL; AK002305; BAB14008.1; -.
EMBL; AK022305; BAB14008.1; -.
EMBL; AL355192; CAB90248.1; -.
EMBL; Z98743; CAB11416.1; ALT_INIT.
EMBL; Z98743; CAB11416.1; ALT_INIT.
EMBL; Z83838; CAB62993.1; ALT_INIT.
PIR; B59436; B59436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:677; ARHGAPB.
InterPro; IPR001251; CRAL_TRIO.
InterPro; IPR000198; RhoGAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PS50191; CRAL_TRIO; 1.
PROSITE; PS50238; RHOGAP; 1.
lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                    Name=4;
IsoId=Q9NSG0-5;
                                                                                                   IsoId=Q9NSG0-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                               Name=2;
                                                                                                                                                                                                                                                                                                          Маше≖5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=7
                                                                             Name=1
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                                                                                                                             LESTHERLEXPOLVIPPEVLRYDER -> QEPPCQANTLVL
KGPDSQHFFRAGILLYCNNSAGLCSSKTLWTLKCEFHVIFT
CHEIFFCFFFSTT (in isoform 2).
/FTId=VSP_001653.
Missing (in isoform 4 and isoform 7).
/FTId=VSP_001654.
Missing (in isoform 2).
/FTId=VSP_001655.
V -> A (in isoform 6).
/FTId=VSP_001656.
Missing (in isoform 6).
/FTId=VSP_001656.
Missing (in isoform 6).
/FTId=VSP_001656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myogenesis
                                          /FTId=VSP_001651.
Missing (in isoform 1 and isoform 6).
/FTId=VSP_001652.
YKKNLKALYVVHPTSFIKVLWNILKPLISHKFGKKVIYFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Genet. 93:284-zyu(zvvz).
ON: Transcriptional repressor. Inhibits myogenesis.
T: Efficient DNA binding requires dimerization with another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JJR7;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Achaete-scute homolog 3 (bHLH transcriptional regulator Sgn-1) (Mash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=21643927; PubMed=11784080;
Yoshida S., Ohbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
"Sgn1, a basic helix-loop-helix transcription factor delineates the salivary gland duct cell lineage in mice.";
Dev. Biol. 240:517-530(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICITY: Specifically expressed in the salivary duct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zabel B., Hankeln T., Schmidt E.R.;
"Comparative genomic sequencing reveals a strikingly similar architecture of a conserved syntenic region on human chromosome 11p15.3 (including gene ST5) and mouse chromosome 7.";
Cytogenet. Cell Genet. 93:284-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kemp P.R., Cooper W.N., Metcalfe J.C.;
Kemp P.R., Cooper W.N., Metcalfe J.C.;
"MASH3 a novel basic helix-loop-helix protein that inhibits
in C2C12 cells.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                            7181835625487465 CRC64;
                   (in isoform 3). SP_001651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DF
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |:||:||:||:
RRSASVQTVREIQRL 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLSQEQLEHRERSLQTLRDIQRM 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCL3 OR MASH3 OR SGN1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                81953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDARD;
                                                                                                                                                                                                                                                                                                                                               579
                                                                                                                                                                                                                                                                                                                                                                                             718
                                                                       382
                                                                                                                                                                                                                                                                                              718
                                                                                                                    451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
MEDLINE=21418998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Efficients below to subcellular LO TISSUE SPECIFIC cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ST
                                                                                                                                                                                                                                                                                                                                                                                                                                              718 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLRTEGLF
                                                                                                                                                                                                                                                                                                                                                                                           580
                                                                       355
                                                                                                                      386
                                                                                                                                                                                                                                                                                              452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
ASH3_MOUSE
ID ASH3_MOUSE
AC Q9JJR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                       VARSPLIC
                                                                                                                                                                                                                                                VARSPLIC
                                                                         VARSPLIC
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rice seedling shoots.";
Mol. Genet. 225:305-313(1991).
-!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                         REMEL; AB04654...
REMEL; AB04654...
REMEL; AJ400878; CAB942...
REMEL; AJ400878; CAB942...
REMEL; AJ400878; CAB942...
REMEL; AJ400878; CAB942...
REMEL; AJ400878; CABSOR.
REMEL; AJ400853; Canucleus; IDA.
DR GO; GO:0005567; Catranscription factor complex; IPI.
DR GO; GO:0005515; Fibratein binding activity; IDA.
DR GO; GO:000557; P:regulation of transcription from Pol II pro. ..; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. ..; IDA.
DR PROSITE; PS00038; HLH.1.
DR RAMRT; SM00353; HLH.1.
DR ROSITE; PS50888; HLH.2; 1.
DR PROSITE; PS50888; HLH.2; 1.
        QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
BASIC HELIX-LOOP-HELIX (BHLH) FAMILY SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dehesh K., Tepperman J., Christensen A.H., Quail P.H.; phyB is evolutionarily conserved and constitutively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: || | ::||| ::||| | LPEDYLEKRLSKVETLRAAIKYISYLQSLLYPDESE 154
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MEDLINE-91172131; PubMed-2005872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSQEQLEHRERSLQTLRD-----IQRMLFPDEKE
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytochrome B.
PHYB OR PHYB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.6%; Score 54.5; Dilarity 36.1%; Pred. No. 3.5; Conservative 7; Mismatches
     SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTORS. ASC
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ277605; CAC37689.1; -. EMBL; AB046448; BAB83911.1; -. EMBL; AJ400878; CAB92296.1; -.
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Les 13; Conserv
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P25764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
 SUBUNIT: Homodimer.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYTOCHROME_1; 1.
PHYTOCHROME_2; 1.
ulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMOPHORE (BY SIMILARITY). IN; E8292E88B769BF16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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PAS 2.
HISTIDINE KINASE.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
protein yqqT.
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Pred. No. 30;
4; Mismatches
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|ERDLQLIRDI-----PDE 1040
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                                                                                                                                                                                                                                                                                                                  594; ATPbind_ATPase.
018; GAF.
561; His_kinA.
167; His_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; sensory_box;
HIS_KIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8969508;
                                                                                                                                                                                                                                                                                                                                                                                  67; His_kinase.
14; PAS_domain.
94; Phytochrome.
                                                                                                                                                                                                                                                                                                                     InterPro; PR003594; ATPbind_AT InterPro; IPR003594; ATPbind_AT InterPro; IPR003561; His_kina.
InterPro; IPR003661; His_kina.
InterPro; IPR001294; Phytochron Pfam; PF01590; GAF; 1.
Pfam; PF05129; HATPase_c; 1.
Pfam; PF00512; Hiska; 1.
Pfam; PF00512; Hiska; 1.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00360; Phytochrome; 1.
PRNRT; SM00387; HATPase_c; 1.
SMART; SM00089; PAS; 2.
TIGRFAMS; TIGR00229; Sensory_bc PR0SITE; PS50109; HIS_KIN; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50125; PHYTOCHROME_1 PROSITE; PS50125; PHYTOCHROME_1 PROSITE; PS50125; PHYTOCHROME_1 PROSITE; PS50046; PHYTOCHROME_1 PROSITE; PS50046; PHYTOCHROME_1 PROMAIN 661 732 PPUDMAIN 795 866 PPUDMAIN 795 866 PPUDMAIN 394 364 CH SEQUENCE 1171 AA; 128384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iAF; 1.
IATPase_c; 1.
IisKA; 1.
                                                                                                                                                                                                                                                                   EMBL; X57563; CAA40795.2; -. PIR; S14065; S14065. Gramene; P25764; -.
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48.1%;
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YQGT_BACSU
ID YQGT_BACSU
AC P54497;
DT 01-OCT-1996 (Rel. 3.
DT 01-OCT-1996 (Rel. 3.
DT 28-FEB-2003 (Rel. 4.
DE HYPOTHETICAL Protein
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STRAIN=168 / JH642;
MEDLINE=97124195; P
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Best Local Similarity
Matches 13; Conser
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Runst National C. V. Moszer I., Albertini A.M., Alloni G.,

Runst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Runst F., Ogasawara N., Moszer I., Albertini A.M., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Bornise R., Boursier L., Connerton I.F., Cummings N.J., Daniel R.A.,

Rhian K.D., Errington J., Pabret C., Ferrari B., Foulger D.,

Rhian K.D., Errington J., Pabret C., Ferrari B., Foulger D.,

Rritz C., Fujita M., Fujita Y., Fuma S., Galizzi, A., Galleron N.,

Rhibert H., Bolsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,

A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Rhibert H., Bolsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Glene C.,

Robayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,

Robayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,

Robayashi Y., Koetter P., Mizuno M., Mosetl D., Nakai S., Noback M.,

Robayashi Y., Koetter P., Mizuno M., Mosetl D., Nakai S., Noback M.,

Robayashi Y., Koetterle D., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

Ra Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

Rato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Schiquchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

Radeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takamaru K.,

Winters P., Wipat A., Yanamoto H., Yanane K., Yasumoto K., Yasa K.,

Winters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yasa K.,

Wanthers P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yasa K.,

Ray Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Ray Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Ray Yoshida K., Yoshikawa H.F., Zumstein P., Yoshikawa H., Danchin A.,

Ray Yoshida K., Yoshikawa H.F., Zumstein P., Yanane M.,

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Kobayashi Y.; *Systematic sequencing of the 283 kb 210 degrees-232 degrees region the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
-!- SIMILARITY: STRONG, TO B.SPHAERICUS GAMMA-D-GLUTAMYL-L-DIAMINO
ACID ENDOPEPTIDASE I (EC 3.4.99.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 AA; 43439 MW; 1075CDC124823BB4 CRC64;
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4: Mismatches
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13;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M14.008; -. Subtilist; BG11687; yqgT. InterPro; IPR000834; Zn_carbOpept. Pfam; PF00246; Zn_carbOpept; 1. PRINTS; PR00765; CRBOXYPTASEA.
                                                                                                                                                           Microbiology 142:3103-3111(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHSCKELQTIQDIKRFLQP 68
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52.6%;
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Best Local Similarity 52....
Local Similarity 52....
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Kuramitsu S.;
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Best Local Simi
Matches 11;
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DOMAIN
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                                                                                                                                                                                                                                                                                                           STRAIN=GK24;
Nashiru O., Park B.C., Ko J.H., Kim J.S., Koh S.K., Lee H.C.,
Kim C.H., Lee S.Y., Lee D.-S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a weak ATPase activity (By similarity).
-!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                        Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 1; Length 817;
Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodoui; rootto, SMART; SM0534; MUTSac; 1.
SMART; SM00533; MUTSd; 1.
TIGREAMS; TIGR01070; mutSl; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
DNA repair; ATP-binding; DNA-binding.
NP_BIND 589 596 ATP (POTENTIAL).
O17 AA: 91179 MW; 61EA066FB84BA761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTS_THETH STANDARD; PRT; 818 AA. Q56239; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) DNA mismatch repair protein muts.
                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA mismatch repair protein muts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKVPQEYRPVQTLKDRQRYTLPEMKE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQLEHRERSLQTLRDIQRMLFPDEKE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF007553; AAD01407.1; -. HAMAP; MF_00096; -; 1. InterPro; IPR005748; Muts1. InterPro; IPR000432; Muts_C. InterPro; IPR002863; Muts_C. Pfam; PF01624; Muts_I; 1. Pfam; PF05198; Muts_Ii; 1. Pfam; PF05192; Muts_Iii; 1. Pfam; PF05190; Muts_Iii; 1. Pfam; PF05190; Muts_Iii; 1. Pfam; PF000188; Muts_V; 1. ProDom; PD001263; Muts_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%;
42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42....
Best Local 11; Conservative
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus thermophilus.
Bacteria, Deinococcus
                                                                                                                                                                     MUTS.
Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires
or send an email
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                    NCBI_TaxID=272;
                                      MUTS_THECA
Q9ZIX6;
30-MAY-2000 (
30-MAY-2000 (
28-FEB-2003 (
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MUTS_THETH
   RESULT 9
MUTS_THECA
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                                             HD DATE DATE OF SOCION ON SOCION OF 
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                                                                                                                                                                                                                                                                                                                                                         "Domain organization and functional analysis of Thermus thermophilus MutS protein.";
Nucleic Acids Res. 26:4153-4159(1998).
-!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a maximal ATPase activity at 80 degrees Celsius. Binds double-stranded DNA.
-:- SUBUNIT: Homotetramer.
-:- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                        DOMAIN STRUCTURE.
STRAIN=HB8 / ATCC 27634;
MEDLINE=98391738; PubMed=9722634;
Tachiki H., Kato R., Masui R., Hasegawa K., Itakura H., Fukuyama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASHINGAN STANDARD;
O9NQ33; UBWYQ6;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                     thermoph11ic
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SEQUENCE FROM N.A., SEQUENCE OF 1-20, AND CHARACTERIZATION. STRAIN=HBB / ATCC 27634;
MEDLINE=96177563; PubMed=8604304;
Takamatsu S., Kato R., Kuramitsu S.;
"Mismatch DNA recognition protein from an extremely thermog bacterium, Thermus thermophilus HBB.";
Nucleic Acids Res. 24:640-647(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P (POTENTIAL).
657FD676BF033506 CRC64;
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B; DNA-BINDING.
C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53; DB :
Pred. No. 31;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO1070; muts1; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2;
DNA repair; ATP-binding; DNA-binding.
INIT_MET 0 0
DOMAIN 1 129 A1.
DOMAIN 130 273 A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:: |:||:||:|| |: || EKVPQEYRPVQTLKDRQRYTLPEMKE 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00096; -; 1.
InterPro; IPR005748; MutS1.
InterPro; IPR005748; MutS1.
InterPro; IPR002863; MutS_C.
InterPro; IPR002863; MutS_N.
Pfam; PF01624; MutS_I; 1.
Pfam; PF05192; MutS_I; 1.
Pfam; PF05192; MutS_II; 1.
Pfam; PF05190; MutS_II; 1.
Pfam; PF05190; MutS_II; 1.
Pfam; PF00488; MutS_V; 1.
ProDom; PD001263; MutS_C; 1.
SMART; SM00534; MUTSac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91249 MW;
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1; Conservative
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129
273
569
818
597
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274
570
590
818 AA;
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NCBI_TaxID=76856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-VF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. ASC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                               ECUENCE FROM N.A.
MEDLINE=21643927; PubMed=11784080;
Yoshida S., Ohbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
"Sgn1, a basic helix-loop-helix transcription factor delineates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00038; HLH_1; 1.

PROSITE; PS50888; HLH_2; 1.

Transcription regulation; Repressor; DNA-binding; Nuclear protein.

DNA_BIND 95 105 BASIC DOMAIN.

DOMAIN 106 145 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).

CONFLICT 54 54 R -> L (IN REF. 1).
                                                                                                                                                                                                                      salivary gland duct cell lineage in mice.";
Dev. Biol. 240:517-530(2001).
[2]
SEQUENCE FROM N.A.
MEDLINE=21418998; PubMed=11528127;
Amid C., Bahr A., Mujica A., Sampson N., Bikar S.E., Winterpacht Zabel B., Hankeln T., Schmidt E.R.;
"Comparative genomic sequencing reveals a strikingly similar architecture of a conserved syntenic region on human chromosome 11p15.3 (including gene ST5) and mouse chromosome 7.";
Cytogenet. Cell Genet. 93:284-290(2001).
-1- FUNCTION: Transcriptional repressor. Inhibits myogenesis (By
                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41, Created)
41, Last sequence update)
41, Last annotation update)
g factor (Ribosome releasing factor) (RRF)
                   (Human).
!tazoa; Chordata; Craniata; Vertebrata; Eutele
!heria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .eatum (subsp. nucleatum).
.eria; Fusobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.5%; Score 52.5; Di
36.1%; Pred. No. 6.6;
vative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB046450; BAB83913.1; -.
EMBL; AJ400877; CAB92288.1; ALT_INIT.
Genew; HGNC:740; ASCL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:740; ASCL3.
InterPro; IPR001092; HLH_basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
Ribosome recycling
FRR OR FN1623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00110; HLH; SMART; SMO0353; HLH PROSITE; PS00038; PROSITE; PS50888; I
                                        Eukaryota; Metazoa
Mammalia; Eutheria
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Best Local Similarity
Matches 13; Conser
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Bacteria; Fusobact
Fusobacterium.
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180
                                                                             NCBI_TaxID=9606;
                        Homo sapiens
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Q8R5Z9;
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 OR
 ASCL3
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AC AC DIT DIT OC OC OC OC
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SEQUENCE FROM N.A.

STRAIN=ATC 25586;

MEDLINE=21886394; PubMed=11889109;

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

A vasleva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Fonstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium

"Genome sequence and analysis of the oral bacterium Fusobacterium

"J. Bacteriol. 184:2005-2018(2002).

"L. FUNCTION: Responsible for the release of ribosomes from messenger

RNA at the termination of protein biosynthesis. May increase the

efficiency of translation by recycling ribosomes from one round of

translation to another (By similarity).

-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-:- SIMILARITY: BELONGS TO THE RRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ı,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
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Interpro; IPR002661; RRF.
Pfam; PF01765; RRF; 1.
ProDom; PD004103; RRF; 1.
TIGRFAMS; TIGR00496; frr; 1.
Protein biosynthesis; Complete proteome.
SEQUENCE 190 AA; 21438 MW; 81BD4A7A293B2814 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.5;
Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE010470; AAL93738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.5%;
36.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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hes 13; Conser
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to license@isb-sib.ch)

Wed

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"Complete genomic sequence of the filamentous nitrogen-fixing
 an email
 send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPSB_ANASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).
                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phytochrome B.";
Plant Physiol. 113:611-619(1997).

-!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOTE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homodimer (By similarity).
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 208-11/0 FIGURE SEQUENCE OF 208-11/0 FIGURE STRAIN=CV. 58M;

MEDLINE=97198556; PubMed=9046599;

Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,

Morgan P.W., Mullet J.E.;

The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

The 113:611-619(1997).

The PORM THAT AB
                                                                                                                                                                                                                                                                                                                                                              (Sorghum) (Sorghum vulgare).
liplantae; Streptophyta; Embryophyta; Tracheophyta;
Aagnoliophyta; Liliopsida; Poales; Poaceae;
nnicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on P.M., Cordonnier-Pratt M.-M., Pratt L.H.; gene family in tomato and the rapid differential family in angiosperms."; 17:362-373(2000).
                                                                                                                                                 1;
                                                                                                                     Score 52.5; DB 1; Length 242; Pred. No. 9.2;
                                                                                                                                                 Indels
                                                    EMBL; AE000706; AAC06923.1; -.
PIR; B70366; B70366.
Hypothetical protein; Complete proteome.
SEQUENCE 242 AA; 28618 MW; CE2C25680D721E93 CRC64;
                                                                                                                                                 5
                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     1178 AA
                                                                                                                                                7; Mismatches
                                                                                                                                                                          10 HRERSLQT-LRDIQRMLFPDEKEF 32
                                                                                                                                                                                         |: ||: :|:|| |||| HRTSLRKFVREIEKMVFEAEKEF 83
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10723737;
                                                                                                                      29.5%;
                                                                                                                                                  vative
                                                                                                                                                                                                                                                                     ANDARD;
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P93527;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
28-FEB-2003 (Rel. 4
Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor (Sc
Eukaryota; Viridip
Spermatophyta; Magi
PACCAD clade; Pani
                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conser
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 modified and this
entities requires
or send an email t
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A STRAIN=CV. 58M; MEDLINE=20188796;
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Sorghum bicolor
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PHYB_SORBI
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Brahamsha B., Haselkorn R.; "Identification of multiple RNA polymerase sigma factor homologs in the cyanobacterium Anabaena sp. strain PCC 7120: cloning, expression, and inactivation of the sigB and sigC genes."; J. Bacteriol. 174:7273-7282(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGNO0229; sensory_box; 2.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50046; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
DOMAIN 668 739 PAS 1.
DOMAIN 802 873 PAS 2.
DOMAIN 950 1170 HISTIDINE KINASE.
DOMAIN 23 31 POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOPHORE (BY SIMILARITY). IN; C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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6
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.5; DI
Pred. No. 55;
2; Mismatches
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EMBL; AF182394; AAB41398.2; -.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
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MEDLINE-21595285; Pubmed=11759840;
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                                                               InterPro; PR003661; His_kina.
InterPro; PR003661; His_kinase.
InterPro; IPR00014; PAS_domain.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF0512; HisKa; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00081; HATPase_c; 1.
SMART; SM00081; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=93054341; PubMed=1385387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129136 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%;
ilarity 51.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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54
372
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Plasmid pCC7120alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1178 AA;
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hes 14; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994
01-FEB-1994
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                  Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
-!- SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 52; DB 1; Length 332; 35.5%; Pred. No. 15; tive 6; Mismatches 14; Indels
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Best Local Similarity
Matches 11; Conser
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Search completed: October 15, 2003, 10:31:02 Job time : 6.22179 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 10:27:33; search time 20.2918 Seconds

(without alignments)

445.097 Million cell updates/sec

Title: US-09-915-543-15_COPY_349_383

Perfect score: 178
Sequence: 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q8z8y6 salmonella	Q8zre3 salmonella	Q9nt51 homo sapien	Q9y2h2 homo sapien	Q9vxu1 drosophila	Q9vxu2 drosophila	Q8uca0 agrobacteri	Q8di53 synechococc	Q8izm6 homo sapien	Q8tgz1 methanopyru	Q8vd56 rattus norv	014687 homo sapien	014686 homo sapien	067532 aquifex aeo	Q8prd9 xanthomonas	001302 caenorhabdi
Ω	Q8Z8Y6	Q8ZRE3	Q9NT51	09У2Н2	Q9VXU1	Q9VXU2	Q8UCA0	Q8D153	Q812M6	Q8TGZ1	Q8VD56	014687	014686	067532	Q8PRD9	001302
DB	16	16	₹"	4	Ŋ	S	1.6	16	7	17	11	4	4	16	16	ហ
% Query Match Length DB	1034	1046	859	1132	1208	1398	295	426	433	818	155	4957	5262	227	411	673
% Query Match	32.0	32.0	31.5	31.5	31.5	31.5	30.9	30.9	30.9	30.9	30.1	30.1	30.1	29.8	29.8	29.5
Score	57	57	56	56	56	56	55	55	55	55	53.5	53.5	53.5	53	53	52.5
Result No.		7	ო	4	5	9	7	00	σ	10	11	12	13	14	15	16

Q8w0m3 oryza sativ	Q9htq7 pseudomonas	P87708 fowlpox vir	Q96qe4 homo sapien	Q06407 saccharomyc	Q9j599 fowlpox vir			Q9fpq3 populus tri		yersinia	Q8ff28 escherichia			Q9c975 arabidopsis	O62022 caenorhabdi	Q8iyy3 homo sapien	Q810m4 caenorhabdi	Q8fmb8 corynebacte	Q8xej6 escherichia	Q23995 drosophila	Q9vc47 drosophila	Q24132 drosophila	O56220 mouse mamma	Q9izt3 exogenous m	Q9vn78 drosophila	Q8uvzl brachydanio	Q9fnq6 arabidopsis	Q9hd27 homo sapien
10 Q8W0M3	16 Q9HTQ7	12 P87708	4 Q96QE4	3 Q06407	7	11 Q8BTI8					16 Q8FF28			0	5 062022		_		و	5 Q23995		ø	15 056220	15 Q9IZT3	5 Q9VN78	13 Q8UVZ1	10 Q9FNQ6	4 Q9HD27
399	572	616	946	1009	1766	2607		1151			239			329	337	341	449	848	1047	1464	1464	1464	1755	1755	96	æ	657	675
29.5	29.5	29.5	29.5	29.5	29.5	29.5	28.9	28.9	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.4	28.4	28.4	28.4
52	52	52			52	52	51.5	51,5	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	50.5	50.5	50.5	50.5
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Homo sapiens (Human).
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859 AA;
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NON_TER
SEQUENCE
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09Y2H2
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

RECTRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

LT2.";

LT2.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ATP-dependent dsDNA exonuclease.
SBCC OR STM0395.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
NCBL_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exonuclease; Complete proteome.
SEQUENCE 1046 AA; 117824 MW; BA565CA3BDAD0C82 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
 10;
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                                                                                                                                                                                             1046 AA
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EASLQALTDEEKRLLADQQ 240
                                                                       3 LSQEQLEHRERSLQTLRDIQRMLFPDEK 30
                                            3 LSQEQLEHRERSLQTLRDIQRMLFPDEK 30
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EMBL; AE008713; AAL19349.1; -.

InterPro; IPR003439; ABC_transporter.

InterPro; IPR004592; SbcC.

InterPro; IPR003395; SMC_N.

Pfam; PF02463; SMC_N; 1.

TIGRFAMS; TIGR00618; Sbcc; 1.
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ja_N; 1.
SAC; 1.
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42.9%;
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    vative
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Ottenwaelder B., Ob
Submitted (JAN-2000
EMBL, AL137528; CAE
InterPro; IPR002013
Pfam; PF02383; Syja
PROSITE; PS50275; S
Hypothetical protei
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Best Local Similarity
Matches 12; Conser
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213 LADEQLQQL
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 12;
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   Matches
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Q9NT51
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Q82RE3
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Magase T., Ishikawa K., Suyama M., Nahara O.;
Mayajima N., Tanaka A., Kotani H., Nahara O.;
Myajima N., Tanaka A., Kotani H., Nahara O.;
Mprediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.;
DNA Res. 6:63-70(1999).
EMBL; AB023183; BAA76810.1; -.
InterPro; IPR002013; Syja_N.
Pfam; PF02383; Syja_N; 1.
PROSITE; PS50275; SAC; 1.
Hypothetical protein.
SEQUENCE 1132 AA; 128407 MW; 853719FC0AD455CD CRC64;
                                                                                                                                                               Gaps
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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01-MAY-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG32587 protein.
CG32587 OR CG6350 OR CG7821.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                             31.5%; Score 56; DB 4; Length 859; 33.3%; Pred. No. 76;
1
96781 MW; BCBBC47C8B726D76 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein KIAA0966.
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                                                                                                                                                             Mismatches
                                                                                                                                                                                                                              5 QEQLEHRERSLQTLRDIQRMLFPDEKEFTG 34
                                                                                                                                                                                                                                                                  : | |:| |::| | 317 ENQRSHQELISQLLQSYMKLLLPDDEKFHG
                                                                                                                              Pred. No
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MEDLINE=99246063; PubMed=10231032;
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                                                                                             Query Match 31.5
Best Local Similarity 33.3
Matches 10; Conservative
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RC STRAIN-Berkeley;

RX MEDINE-20190606; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Randon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Miklos G.L.G.,

RA Beeson K.Y., Beanc P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Bortova D., Botchan M.R., Boutler H., Cadieu E., Center A., Chadra I.,

RA Burtis R.C., Busam D.A., Dahlke C., Davemport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Dahlke C., Davemport L.B., Davies P.,

RA Burtis R.C., Busam D.A., Dahlke C., Davemport L.B., Davies P.,

RA Goson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Burtis N.L., Ravley P., Heiman T.J., Herrandez J.R., Heischman W.,

RA Burtis N.L., Harvey D., Heiman T.J., Herrandez J.R., Heischman W.,

RA Burtis N.L., Harvey D., Heiman T.J., Herrandez J.R., Herch D.,

RA Hostin D., Houston K.A., Bowland T.J., Wel M.-H., Ibeywan C.,

A Jalali M., Kalush F., Karpen G.H., Ke.Z., Kennison J.A., Ketchun K.A.,

RA Liu X., Mattei B., McIntosh T.C., McIeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., Morris J., Wesheril A.,

Rak Reiner K., Mey W., Murphy B., Murphy L., Murshy D.M., Nesheeli A.,

Rabon D.R., Nelson K.A., Wixon K., Di J., Liu X., Liu X.,

Reiner S., Jener S., Poller S., Poller S., Schele J.,

RA Bener K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,

Rand S., Wellshin S., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

Rand S., Welber S., Zhon M., Zhong W., Zhong S., Zhu X., Smith H.O.,

Rand S., Welskas R., Zeveri J.S., Zhan M., Zhong W., Zhong S., Zhu X., Smith H.O.,

Rance S., Shore S.
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                                                          Gaps
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                                                                                                                                                                                                                                 Length 1208
Score 56; DB 5; Length 12v
Pred. No. 1.1e+02;
                                                        6; Mismatches
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811 LQQQQAESQEQQASTLRDLERL 832
                                                                                               3 LSQEQLEHRERSLQTLRDIQRM 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:2185-2195(2000).
                31.5%;
ilarity 45.5%;
Conservative
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                   Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Swirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                              Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AE003499; AAF48466.2; -.
EMBL; AY052121; AAF93545.1; -.
FlyBase; FBgn0052587; CG32587.
SEQUENCE 1398 AA; 158484 MW; BBAIC2FE3E9F555D CRC64;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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OBUCAO;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Transcriptional regulator, RpiR family.
ATU2598 OR AGR_C_4707.
Agrobacterium tummefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 5; Length 139
Pred. No. 1.2e+02;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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LQQQQAESQEQQASTLRDLERL 1022
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Stapleton M., Brons
Stapleton M., Chavez (
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Best Local Similarity
Matches 10; Conser
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Misra S., Crosby
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MEDINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
A Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
A Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Flanagan C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
EMBL; AE009106; AAL43579.1; ALT_INIT.
BEBL; AE009173; AAK88321.1;
BEBL; AE008173; AAK88321.1;
BITHERPO; IPR000843; HTH_Laci
BITHERPO; IPR001347; SIS.
BY Fam; PF01418; HTH_E; 1.
BY Pfam; PF01418; HTH_E; 1.
BY Pfam; PF01380; SIS; 1.
BY Pfam; PF01380; SIS; 1.
BY PROSITE; PS00356; HTH_LACI_FAMILY; 1.
                                                                                                             "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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:
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22225144; PubMed=12240834; Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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35;
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PRELIMINARY; PRT; 426 AA.
OBDI53;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Transfer RNA-Gln reductase.
HEMA OR TLL1738.
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AA; 32259 MW; 3B50926B3CB72456 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%; Score 55; DB 40.0%; Pred. No. 35; Live 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 9:123-130(2002).
EMBL; AP005375; BAC09290.1; -.
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                                                                                                                                                                                            Science 294:2317-2323(2001).
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Best Local Similarity
Matches 10; Conserv
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nes 12; Conser
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Q8D153
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014687
                      RESULT 11
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SEQUENCE 1937647; Pubmed-11930014;

RA Sheherbinina O.V., Shakhova V.V., Makarova K.S., Polushin N.N.,

RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

RA Antale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

RA Malykh A.G., Koonin E.V., Kozyavkin S.A.,

RT and monophyly of archaeal methanogens.";

RT and monophyly of archaeal methanogens.";

RT and monophyly of archaeal methanogens.";

RC. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

BR L. EMBL, AEOLO374; AAM02048.1; -.

DR InterPro; IPR001559; AAA_ATPase.

InterPro; IPR001550; Helicase.C.

DR Pfam; PF00271; helicase.C.;

DR Pfam; PF00271; helicase.C.;

DR Pfam; PF00271; helicase.C.;

DR SMART; SM00487; DEXDC; 1.

BRANKT; SM00487; DEXDC; 1.

RW Helicase; Complete proteome.

SO SEQUENCE 818 AA; 91715 MW; C2136200A710817E CRC64;

SEQUENCE 818 AA; 91715 MW; C2136200A710817E Length 818;
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NCBI_TaxID=2320;
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Pred. No. 98;
2; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            Shang X., Zhou Y.T., Low B.C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF544240; AAN40769.1; -.
SEQUENCE 433 AA; 49691 MW; 0AE4B42A404AE1D3 CRC64;
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1; OAE4B42A404AE1D3 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Archaea-specific superfamily II helicase.
MKO835.
Methanopyrus kandleri.
                                                Q8IZM6, PRELIMINARY; PRT; 433 AA. Q8IZM6; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) BCH domain-containing Cdc42GAP-like protein. BPGAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.9%; Score 55; DB 4;
Best Local Similarity 52.2%; Pred. No. 51;
Matches 12; Conservative 4; Mismatches 7
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GLRTEGLFRRSASVQTVREIQRL 246
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Best Local Similarity 54.2%;
Matches 13; Conservative
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SEQUENCE FROM N.A.
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RESULT
Q8IZM6
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-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL; AF010404; AAC51735.1; -.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley;
MEDLINE=21643927; PubMed*11784080;
Yoshida S., Obbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
"Sgn1, a Basic Helix-Loop-Helix Transcription Factor Delineates the
Salivary Gland Duct Cell Lineage in Mice.";
Dev. Biol. 240:517-530(2001).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97388474; PubMed=9247308;
Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative bHLH transcription factor (Fragment).
SGN-1.
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; Pred. No. 28;
7; Mismatches
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36.1%;
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014687;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 36.12,
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26B7C74CAD417E44 CRC64;

564171 MW;

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5262 AA;
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QBPRD9;
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Q8PRD9
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RADINE=97388474; PubMed=9247308;

REDINE=97388474; PubMed=9247308;

REDINE=97388474; PubMed=9247308;

RADINE=97388474; PubMed=9247308;

RADINE=97388474; PubMed=9247308;

RADINELINE AND T., Alder H., Croce C.M., Huebner K., Mazo A.,

RADINELINE AND CALL-1 involved in acute leukemia and to Drosophila setron homology to ALI-1 involved in acute leukemia and to Drosophila rithorax.";

RIT LINEARTY: CONTAINS 1 SET DOMAIN.

REBL; AF010403; AAC51734.1; -.

C -1- SIMILARTY: CONTAINS 1 SET DOMAIN.

REBL; AF010403; AAC51734.1; -.

CREBL; AF010403; RADILZ_DOX.

RITCE-PO: IPR003889; FYICH_N.

RITCE-PO: IPR00310; HMC2_L_DOX.

RITCE-PO: IPR00114; Recombinase.

RITCE-PO: IPR00184; RECOMBINASE.

RITCE-PO: IPR001841; Znf_PHD.

RITCE-PO: IPR001841; RING: 3.

BR SMART; SM001949; RING: 3.

BR SMART; SM0017; SET: 1.

BR SMART; SM0017; SET: 1.

BR SMART; SM0017; SET: 1.

BR PROSITE; PSS0016; ZE-PHD_2; 1.

BR PROSITE; PSS0016; ZE-PHD_2; 1.
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ALR.
ALR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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; RECOMBINASES_2; 1.
); SET; 1.
); ZF_PHD_2; 1.
AA; 531840 MW; 102(
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                     Recombinase.
SET.
Znf_PHD.
      PostSET
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InterPro; IPR003616; Posts; InterPro; IPR006118; Recom! InterPro; IPR001214; SET.
InterPro; IPR001214; SET.
InterPro; IPR001965; Znf_PP Ffam; PF00628; PHD; 3.
Pfam; PF00856; SET; 1.
SMART; SM00541; FYRN; 1.
SMART; SM00541; FYRN; 1.
SMART; SM00249; PHD; 4.
SMART; SM00249; PHD; 4.
SMART; SM00308; PSSET; 1.
PROSITE; PS00398; RECOMBIN PROSITE; PS50280; SET; 1.
PROSITE; PS50280; SET; 1.
PROSITE; PS50280; SET; 1.
PROSITE; PS5016; ZF_PHD_2
SEQUENCE 4957 AA; 53184
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Best Local Similarity
Matches 17; Conse
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014686

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DT 01-JAN-1998 (
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OS ALR.

OS HOMO Sapiens

OC EUWARYOLD HE

OC MAMMAIIA; EUL

OX NCBI_TAXID=96

RN [1]

RA RAIJAPAII R.;

RA RAIJAPAII R.;

RA RAIJAPAII R.;

RA CANAANI E.;

RT "Structure an RT Strong homolog

RT "Strong START; SMO03

REMART; PSSO

REMART; PS
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SEQUENCE FROM N.A.

STEAIN=306 / ATCC 13902 / XV 101;

X MEDLINE=22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Relnach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.E., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Rotmighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
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                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                 ;
    Length 5262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%; Score 53; DB 16; Length 227; 41.4%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                         2396 GLSQTELE-KQRQRQRLRELLIRQQIQRNTLRQEKETAAA 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392:353-358(1998).

EMBL; AE000747; AAC07503.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 227 AA; 27375 MW; 3F9E80A29D606B61 CRC64;
                                                                                                                      35
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC0024.
                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein AQ_1596.
                                                                                                                      2 GLSQEQLEHRERSLOTLRD-----IORMLFPDEKEFTGA
30.1%; Score 53.5; DB 4;
42.5%; Pred. No. 1e+03;
ive 4; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                    227 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 41.4%; Pred. No. 48; nes 12; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QEQLEHRERSLQTLRDIQRML--FPDEKE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gamr
Kanthomonadaceae; Kanthomonas
NCBI_TaxID=92829;
                                Local Similarity 42.5
hes 17; Conservative
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Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; Toomparison of the genomes of two Xanthomonas pathogens with differing host specificities."; Nature 417:459-463(2002).

EMBL; AE011625; AAM34916.1; -. InterPro; IPR002886; Peptidase_M37.

Pfam; PF01551; Peptidase_M37.

Hypothetical protein; Complete proteome.

SEQUENCE 411 AA; 44337 MW; E193496126355426 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                     Query Match 29.8%; Score 53; DB 16; Length 411; Best Local Similarity 36.4%; Pred. No. 89; Matches 12; Conservative 4; Mismatches 17; Indels
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Search completed: October 15, 2003, 10:35:47 Job time: 23.2918 secs

2 GLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTG 34 | | : | | | | | | | | | 1 17 GASAQSQRETERKLQQLRDELKTISADRRELEG 49

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